```
                    1        10        20        30        40        50        60        70        80        90        100
                    |--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
human       MRPQGPAASPQRLRGI--LLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKGEKGECLRESF
mouse       MHPQGRAAPPQLLLGLFLVLLLLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESF
rice_fish          MTPLSPRLLILLCLALPLHGQE--KGRSRGYRKDPDADKF--GSCLQGPAGTPGRDGNPGANGIPGTPGIPGRDGLKGEKGECVSEVF
abra_fish          MGTKLTQLLICFWISLPFCVTQKAKERIPRQ-RDAEFTDKYQA-CVQGVPGVQGRDGNPGINGIPGTPGIPGRDGLKGEKGECVSERF
chicken                                                      RPREVLEAYNGVCLQGPSGVPGRDGNPGTNGIPGTPGIPGRDGPKGEKGECLRESI
consensus          .........ll.......p.......k......r.r#v...yng.ClQGp.GvpGRDGnPG.NGIPGTPGIPGRDG.KGEKGEC1rEsf

                    101      110       120       130       140       150       160       170       180       190       200
                    |--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
human       EESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVE
mouse       EESWTPNYKQCSWSSLNTGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPELNSTINIHRTSSVE
rice_fish   EEPWKPNYKQCAWNSLNYGIDLGKIADCTFTKLRSESALRVLFTGSLRLKCKEACCQRWYFTFDGAECTGPLPVESIIYLNQGSPELNSTINIHRTSSVE
abra_fish   EEPWKPNFKQCAWNSLNYGIDLGKIAECTFTKQRSDSALRVLFSGSLRLKCKTACCQRWYFTFNGAECTGPLPIESIVYLDQGSPELNSTINIHRTSTVE
chicken     EESWTPNFKQCSWSALNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRSACCQRWYFTFNGAECAGPLPIEAIIYLDQGSPELNSTINIHRTSSVE
consensus   EESwtPN%KQCswSsLNYGIDLgKIA#CTFTKnRS#SALRVLFsGSLRLKCr.ACCQRWYFtF#GAEC.GPLP|EaI|YL#QGSPE§NSTINIHRTSSVE

                    201      210       220       230       240     245
                    |--------|---------|---------|---------|-------|
human       GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
mouse       GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
rice_fish   GLCEGIKAGLVDVALWVGTCADYPRGDASTGWNSVSRIIEELPK
abra_fish   GLCEGIHAGLVDVGIWVGTCADYPRGDASTGWNSVSRVIEELPK
chicken     GLCEGINAGLVDIAIWVGTCSDYPRGDASTGWNSVSRIIIEELPK
consensus   GLCEGI.AGLVDi.a|WvGTCsDYPrGDASTGWNSVSR|IIEELPK
```
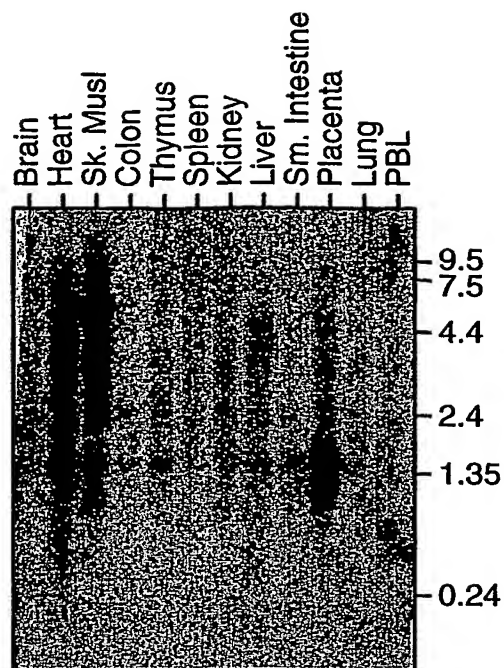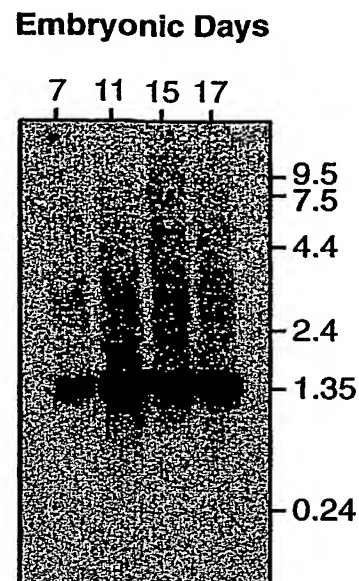
FIG._1

```
         10        20        30        40        50
         |---------|---------|---------|---------|--------|
MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNG
         60        70        80        90        100
MCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNY
         110       120       130       140       150
KQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYF
         170       180       190       200       210
TFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVA
         220       230       240
IWVGTCSDYPKGDASTGWNSVSRIIIEELPK
```
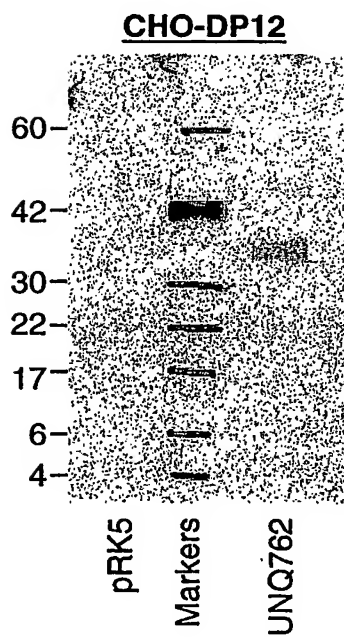
FIG._2
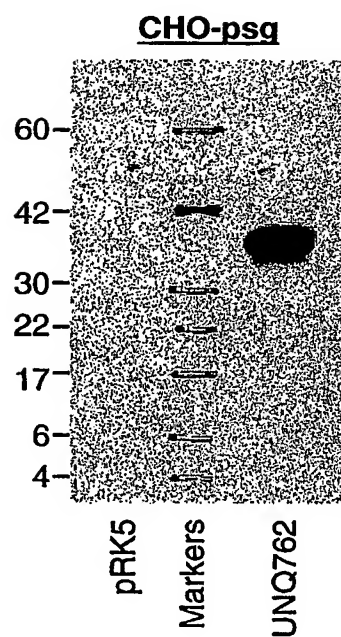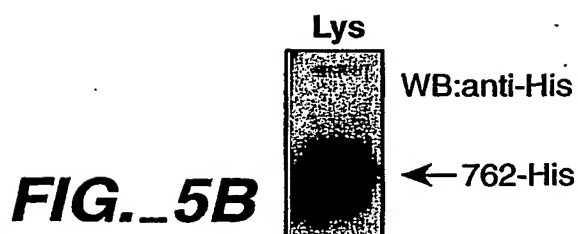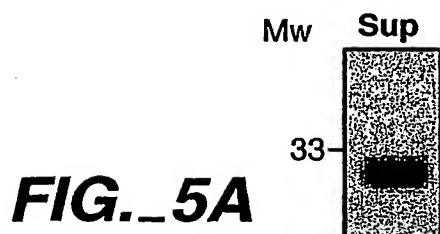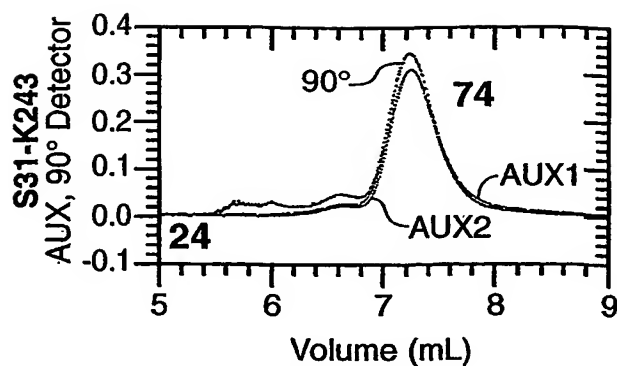
FIG._3A

FIG._3B

FIG._4A
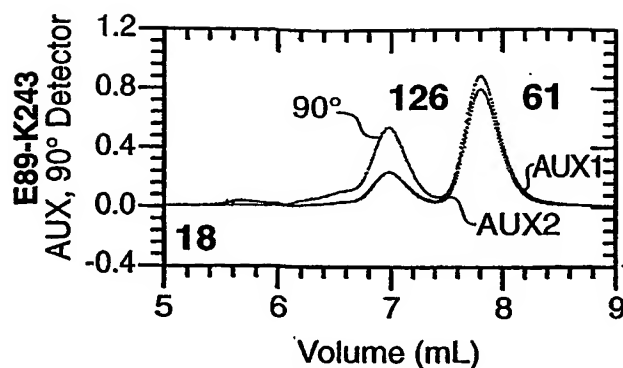

FIG._4B

FIG._5A

FIG._5B

FIG._6A

FIG._6B
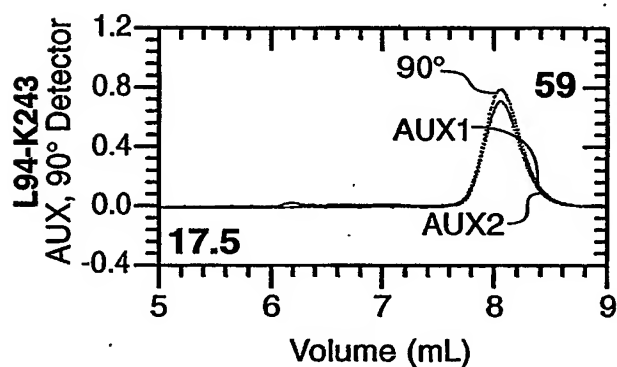
FIG._6C
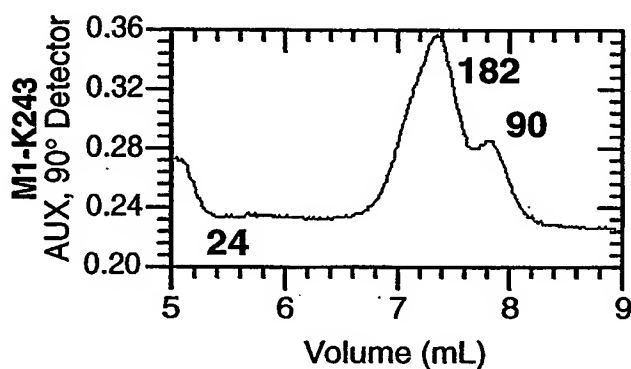
FIG._7A
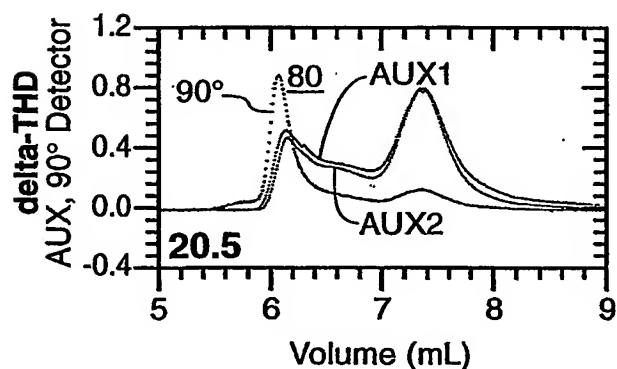
FIG._7B
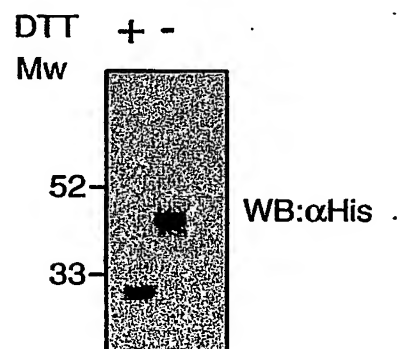
FIG._7C

FIG._8A

FIG._8B

FIG._9A
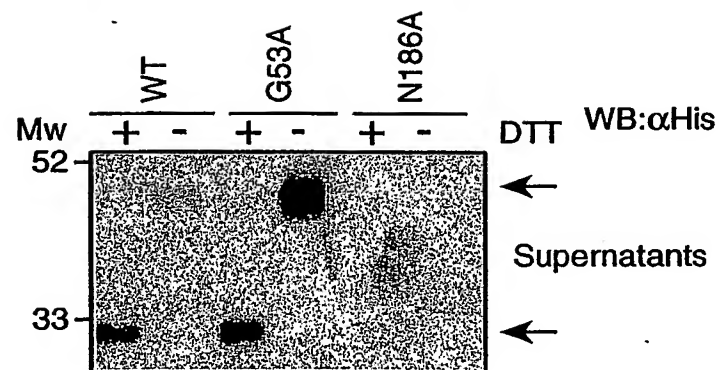
FIG._9B
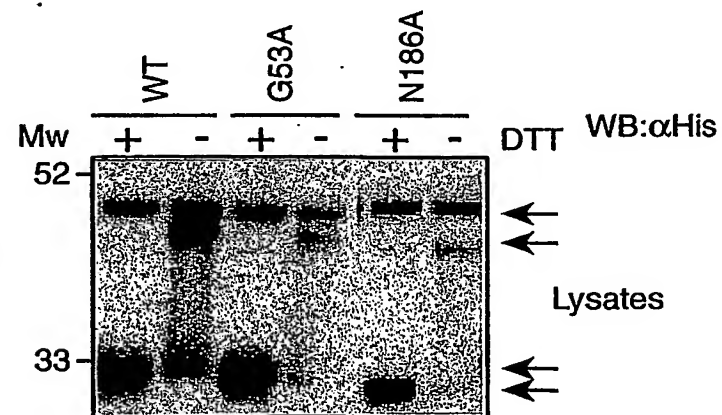
FIG._10A
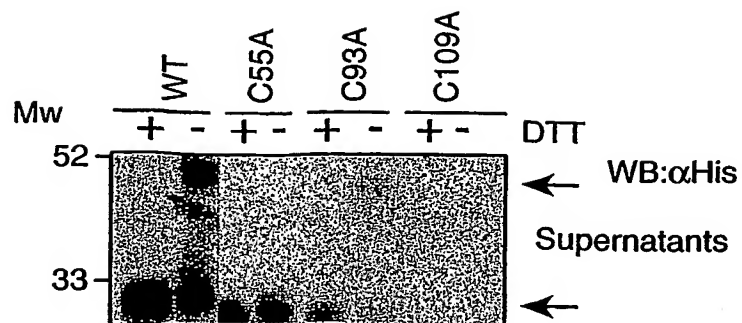
FIG._10B

FIG._11

FIG._12A

FIG._12B

3T3

IP - Whole
Cell Lysates

FIG._13.A

293

IP - Whole
Cell Lysates

← 762
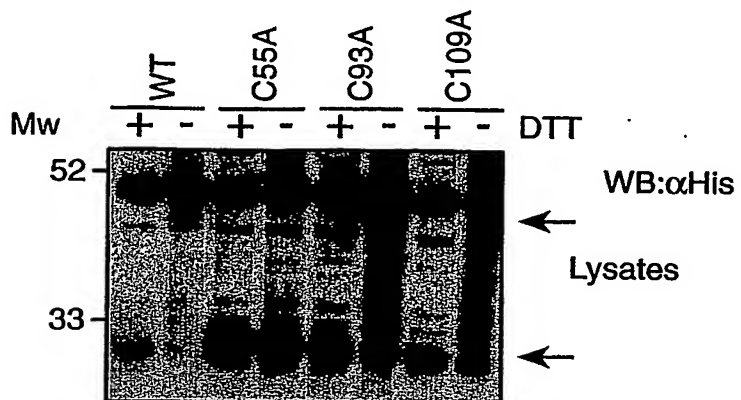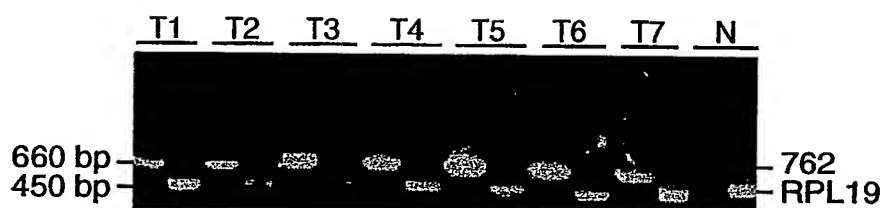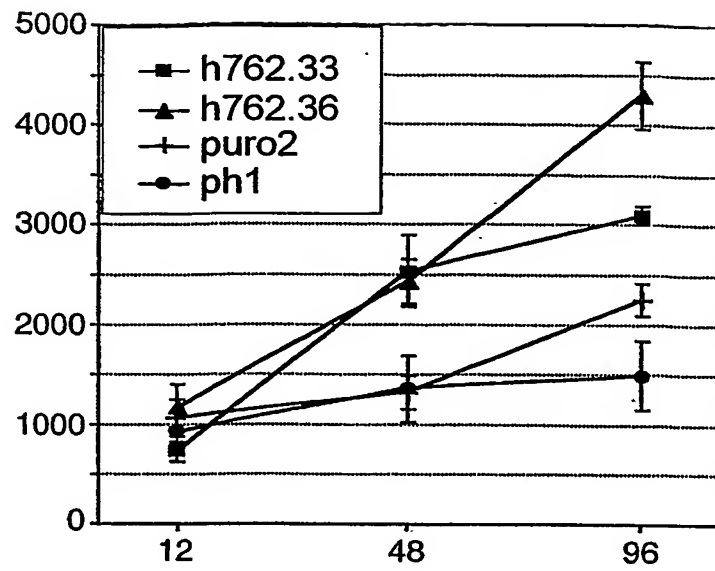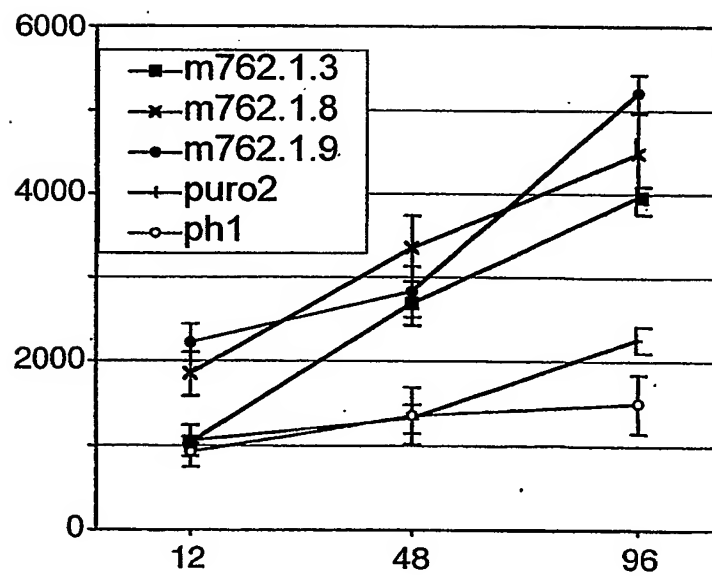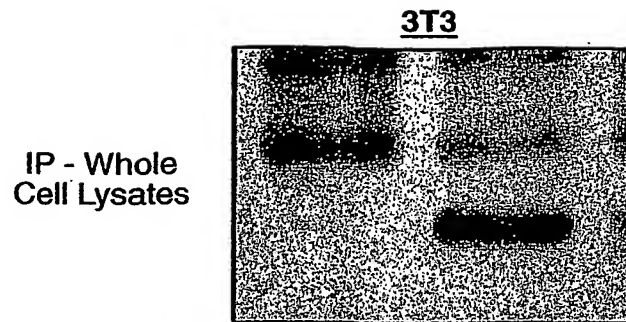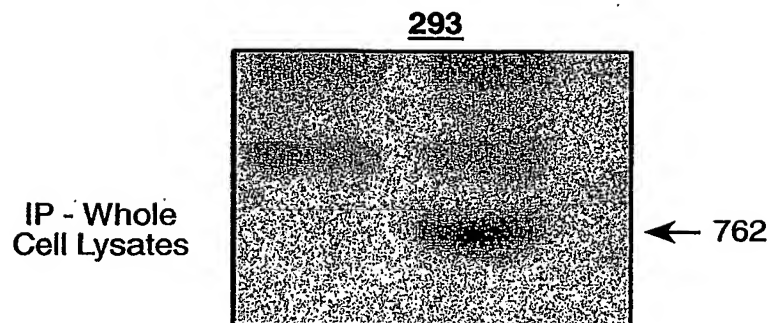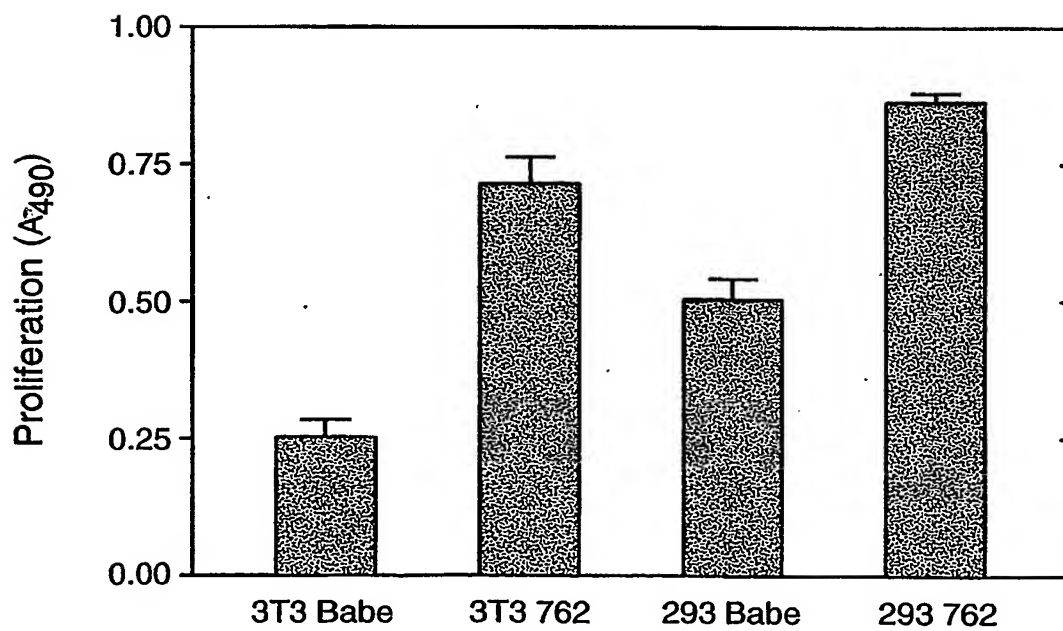
FIG._13.B

FIG._13C
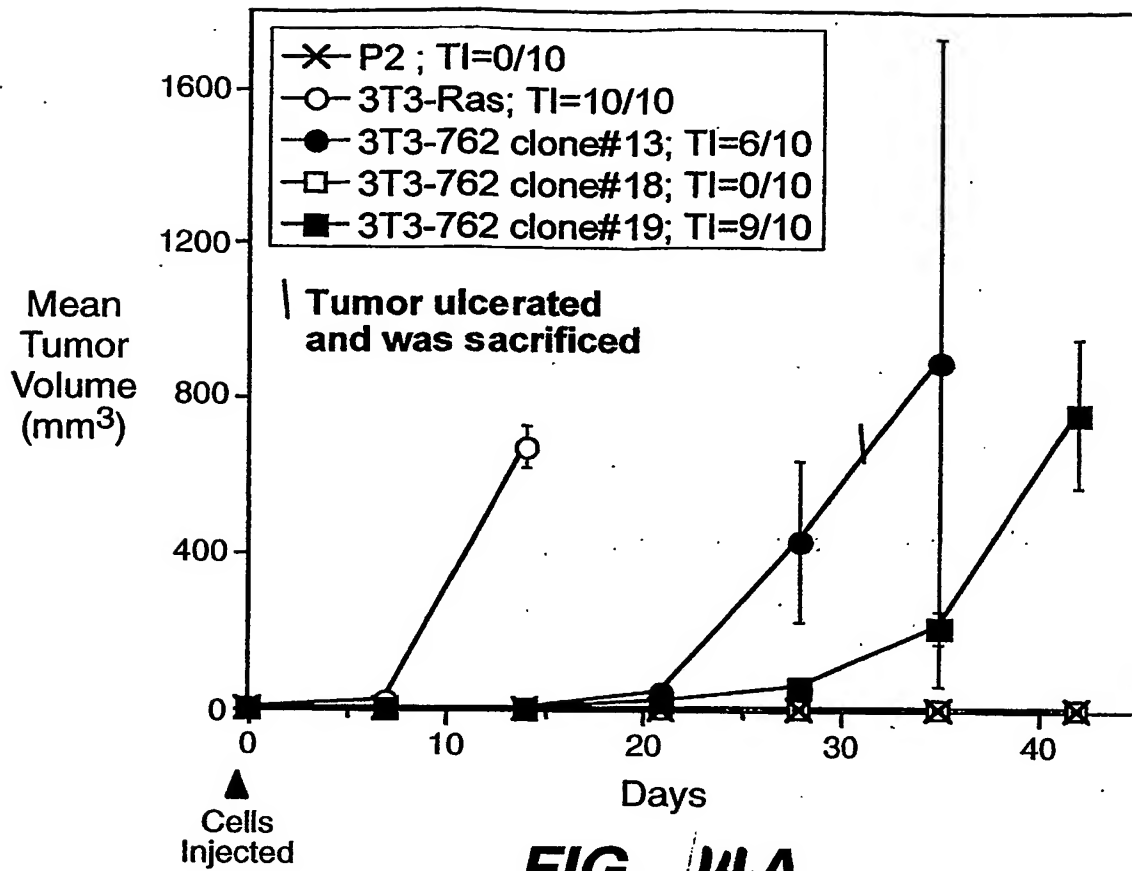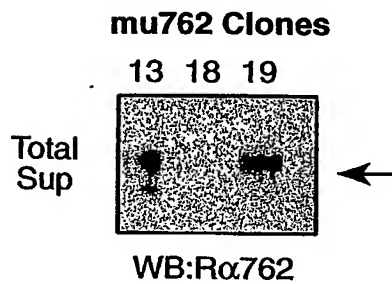
FIG._14A

FIG._14B
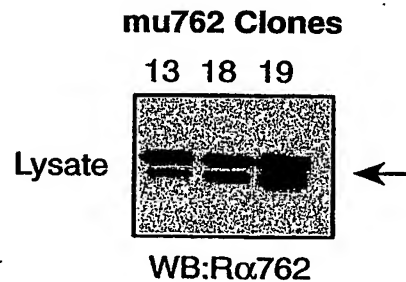
FIG._14C
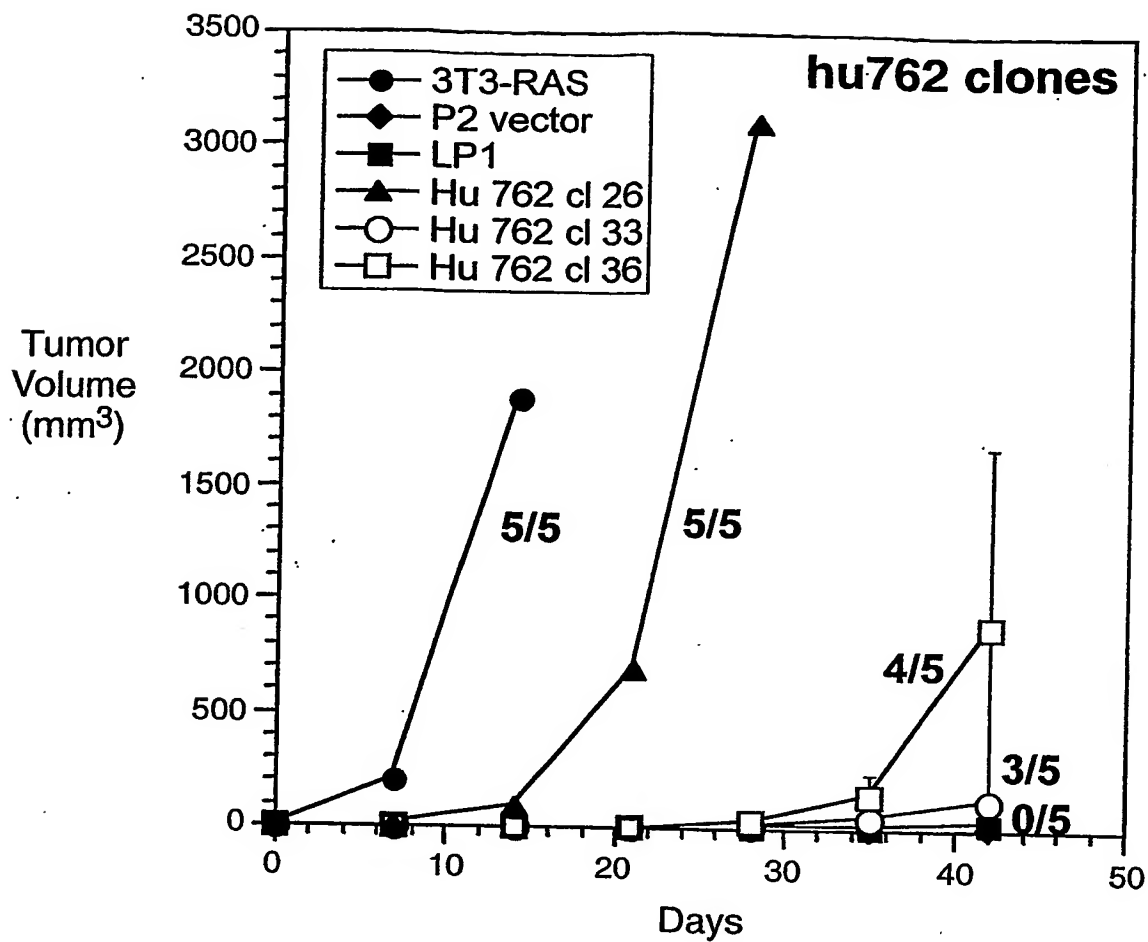
FIG.__ 15
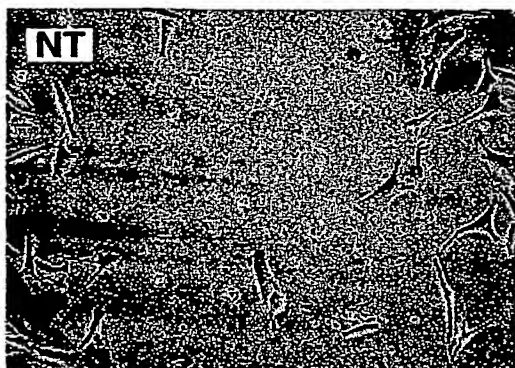
FIG._16 A

FIG._16 C

FIG._16 B

FIG._16 D
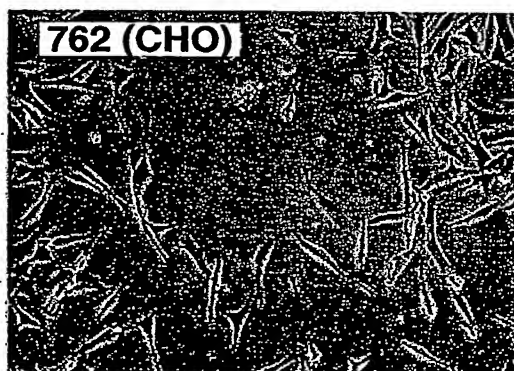
FIG._16 E
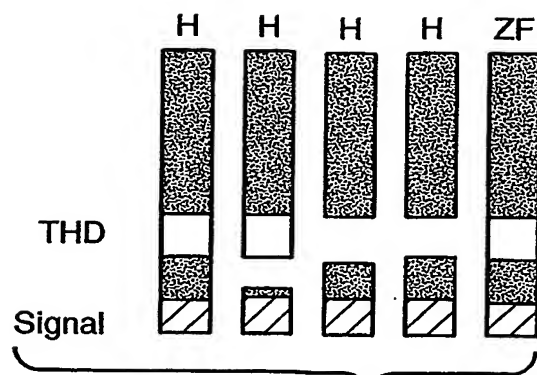
FIG._ 17A
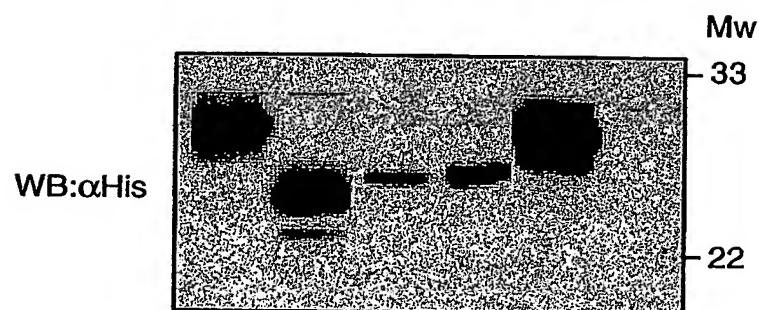
FIG._ 17B
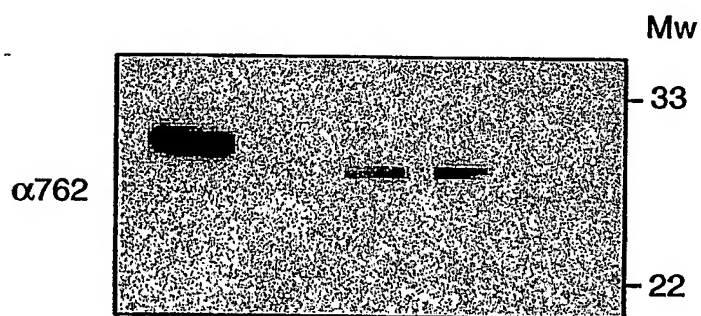
FIG._ 17C

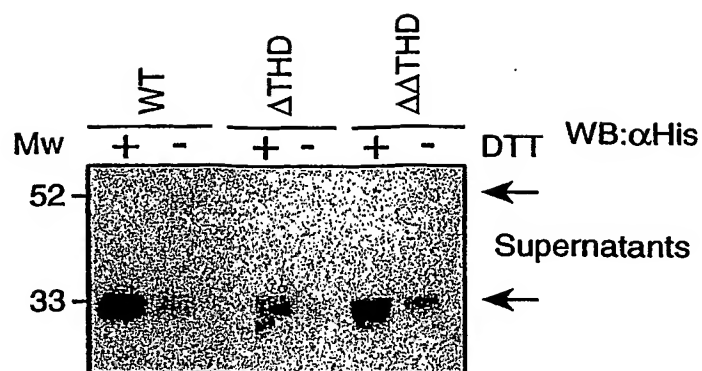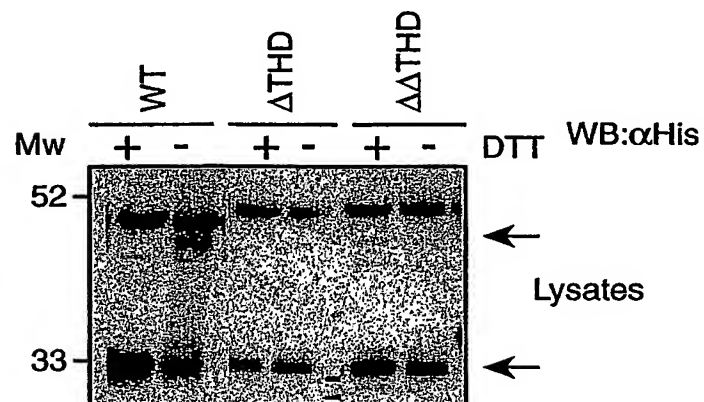|		H1						H2											H3															Name
8	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102				Name
.	I	S	G	S	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	L	-	F	D	Y				S7
.	I	T	N	S	D	A	T	Y	P	P	Y	G	G	Y	T	Y	C	A	R	G	G	G	M	D	G	Y	V	M	D	Y				S16
.	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y				F5
.	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y				F6
.	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y				S4
.	I	S	N	Y	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y				S9
.	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y				F13
.	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y				F47

FIG. 18

	Phage		Fab			IgG	
	762 S/S	762 F/F	762 S/S	762 F/S	762 F/F	762 S/S	762 F/F
S4	3nM	0.9nM	3.6nM (1.9nM)	32nM	13.4nM	0.5nM	3.1nM
S7	35nM	2.7nM	113nM	57nM	n/a	7.3nM	41nM

FIG. 21

FIG._ 19

FIG._ 22

FIG. 20 A

FIG. 20 B

FIG._2B

AP promoter   STII   LC   gD tag   STII   HC   cP3

FIG._24 A

AP promoter   STII   LC   gD tag   STII   HC   LZip   cP3

FIG._24 B

AP promoter   STII   LC   STII   HC
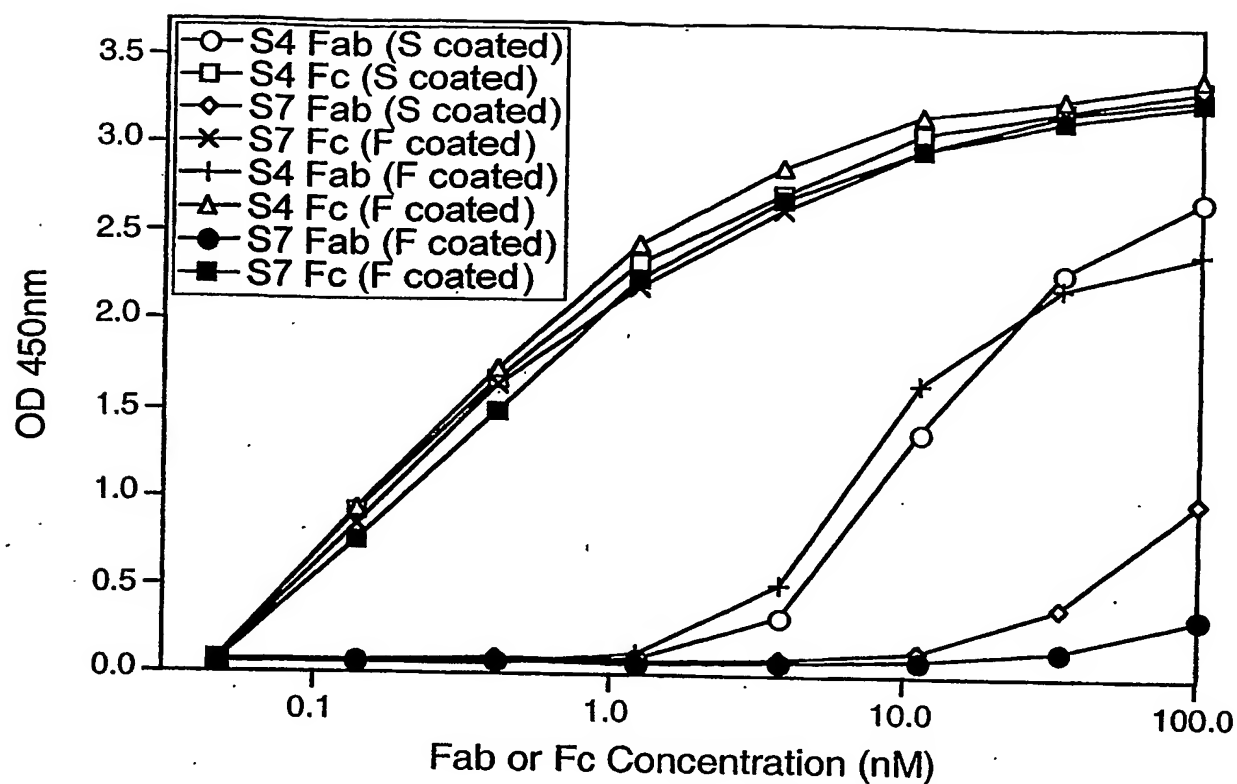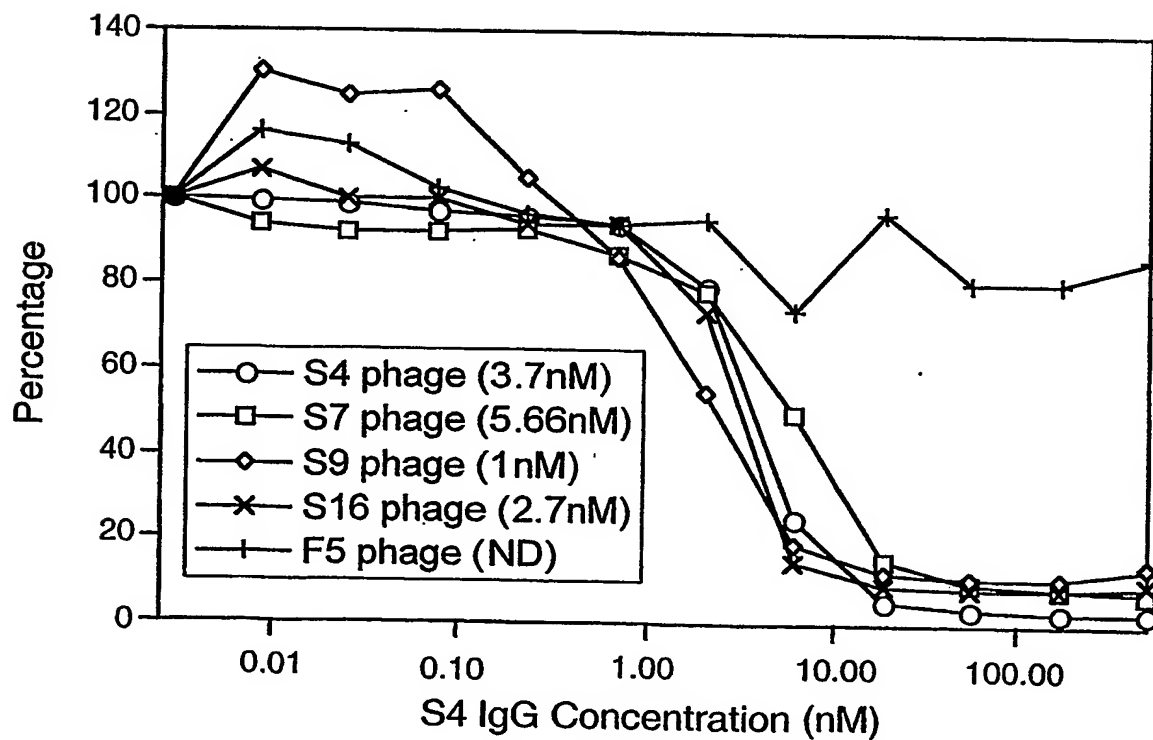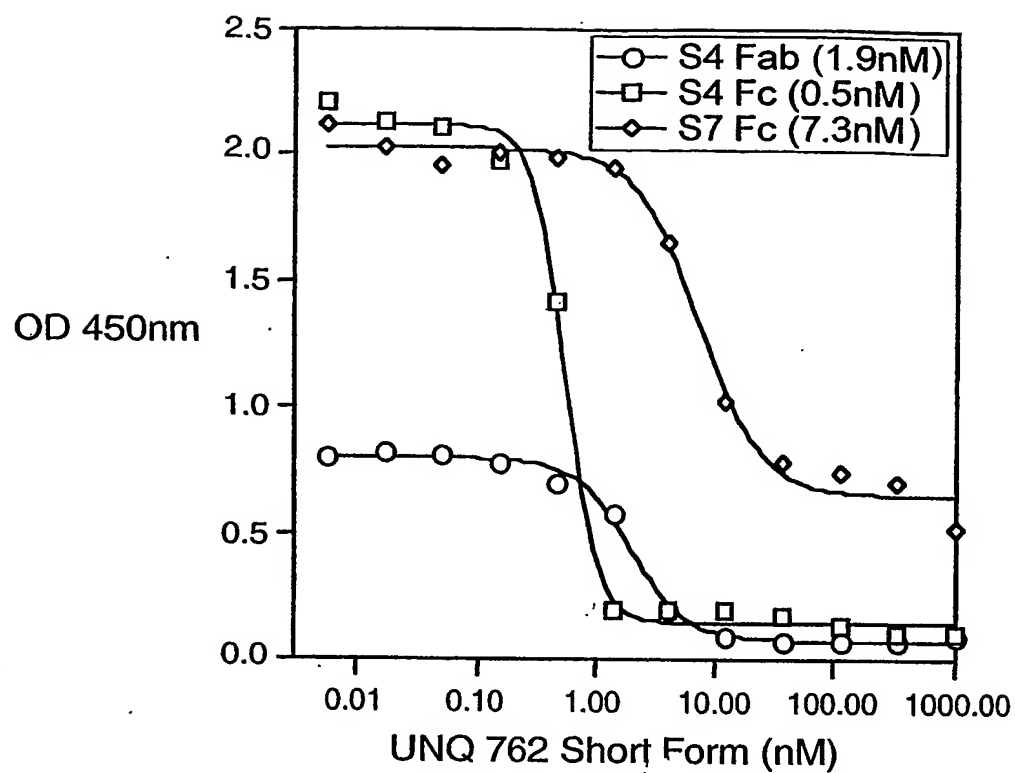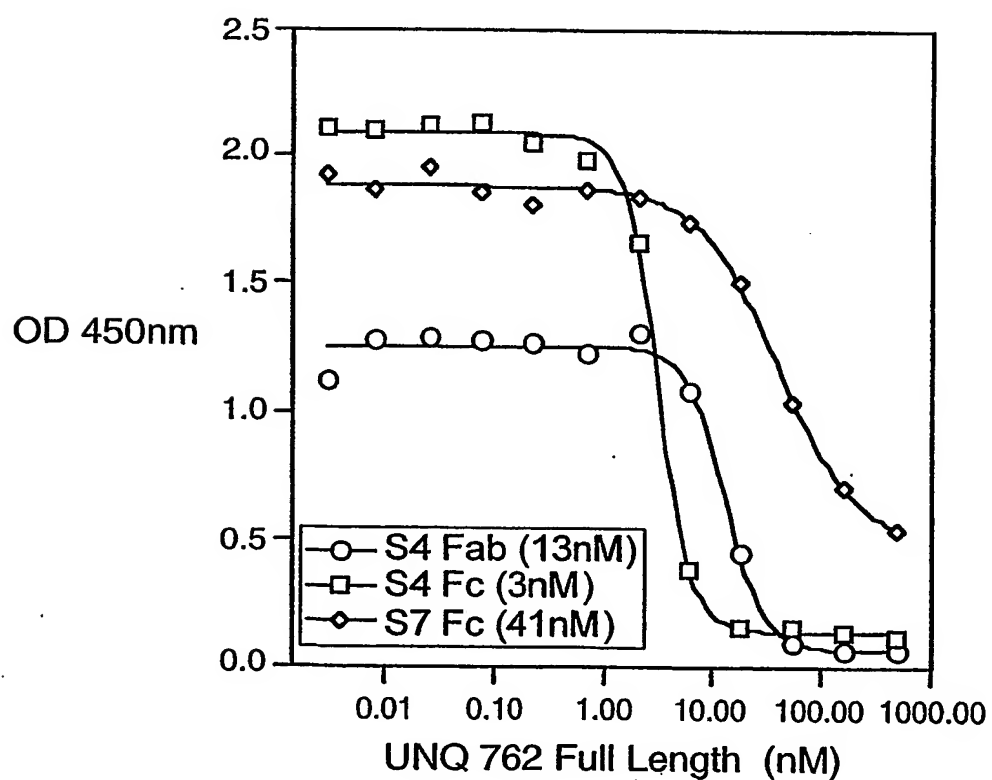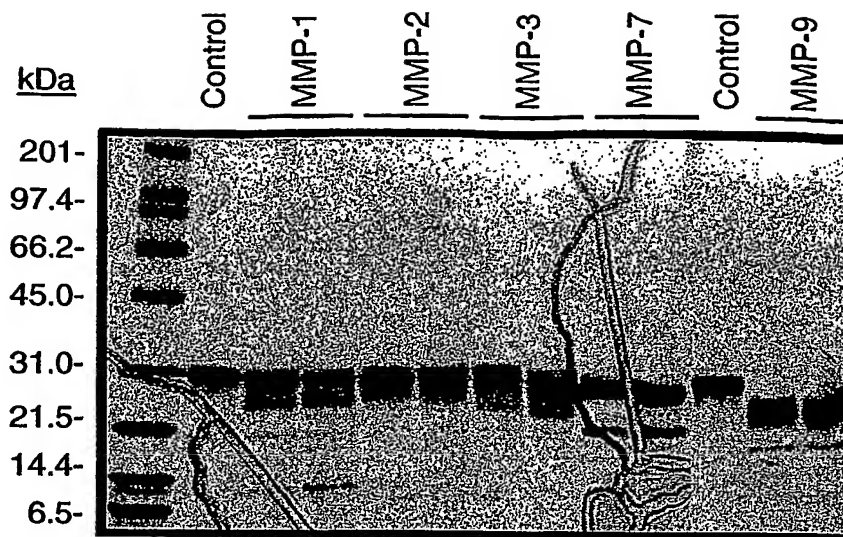
FIG._24 C
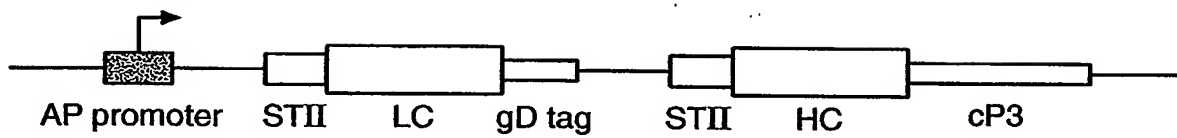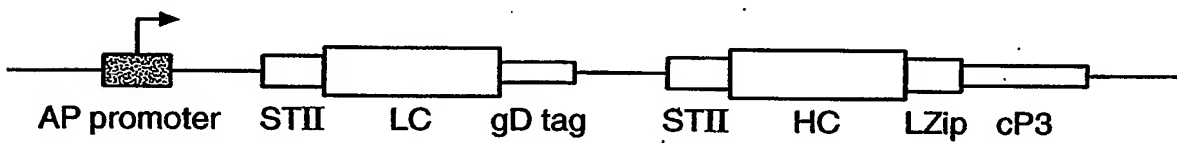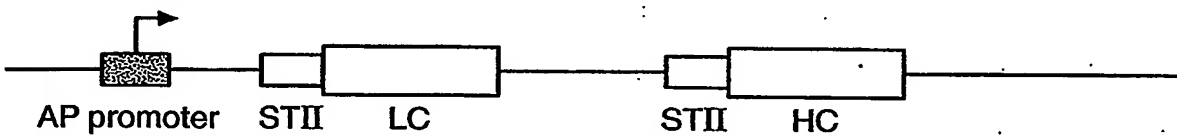
CMV promoter   SS   LC   CMV promoter   SS   HC
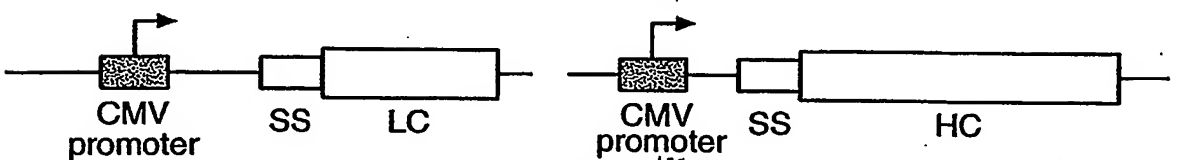
FIG._24 D

```
  1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGAGCTGCTG GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
    TTTTCAATTA GAAAAGTTGT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTTATG AAAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCGTTT TTTCTATTGC TACAAATGCC
    AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAAATAC TTTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
  1                                              M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A
                                                 ^start of stII signal sequence
                                                 ^met

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCCTCTGT GGGCGATAGG GTCACCATCA CCTGCCGTGC CAGTCAGGAT GTGTCCACTG
    ATACGTCTAT AGGTCTACTG GGTCAGGGGC TCGAGGGACA GGCGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCACG GTCAGTCCTA CACAGGTGAC
 22  Y  A  D  I  Q  M  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A
     ^start of light chain                                                            ^CDR-L1

601 CTTGTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCCTCTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
    GACATCGGAC CATAGTTGTC TTTGGTCCTT TTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
 56  V  A  W  Y  Q  Q  K  P  G  K  A  P  K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S
                                               ^CDR-L2

701 CGGTTCCGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTC
    GCCAAGGCCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGGTGCAAG
 89  G  S  G  T  D  F  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  S  Y  T  T  P  P  T  F
                                                                        ^CDR-L3
```

FIG._25A

```
301 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
    CCTGTCCCAT GGTTCCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
122  G  Q  G  T  K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V

901 TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA
    AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG AGGGTCCTCT CACAGTGTCT
156  V  C  L  N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E

901 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT
    CGTCCTGTCG TTCCTGTCGT GGATGTCGGA GTCGTCGTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA
189  Q  D  S  K  D  S  T  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H

.01 CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGCGGT AAGGACCTGG
    GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTCGAGG CCATACCGAC TAGGCTTGGC AAAGGCGCCA TTCCTGGACC
.22  Q  G  L  S  P  V  T  K  S  F  N  R  G  E  C  G  A  S  S  G  M  A  D  P  N  R  F  R  G  K  D  L  A
                                                              ^end of light chain, start of gD tag

.01 CATAAACTCGA GGCTGATCCT CTACGCCCGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
    GTATTGAGCT CCGACTAGGA GATGCGGGCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCCA TTGATCTCCA ACTCCACTAA AATACTTTTT
.56  Q
.23
                                                                                              M  K  K
                                                                                            ^start of stII

01 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGGCTACGC TGAGGTTCAG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG
   CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCCGATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACGTC
20  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  E  V  Q  L  V  E  S  G  G  G  L  V  Q
                                                                         ^start of heavy chain

01 CCAGGGGGGCT CACTCCGTTT GTCCTGTGCA GCTTCTGGCT TCAACATTAA AGACACCTAT ATACACTGGG TGCGTCAGGC CCCGGGTAAG GGCCTGGAAT
   GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
14  P  G  G  S  L  R  L  S  C  A  A  S  G  F  N  I  K  D  T  Y  I  H  W  V  R  Q  A  P  G  K  G  L  E  W
                                       ^CDR-H1
```

FIG._25B

```
1501 GGGTTGCAAG GATTTATCCT ACGAATGGTT ATACTAGATA TGCCGATAGC GTTCACTAT AAGGCCAGAC ACATCCAAAA ACACAGCCTA
     CCCAACGTTC CTAAATAGGA TGCTTACCAA TATGATCTAT ACGGCTATCG CAGTTCCCGG CAAAGTGATA TTCGCGTCTG TGTAGGTTTT TGTGTCGGAT
  48  V  A  R  I  Y  P  T  N  G  Y  T  R  Y  A  D  S  V  K  G  R  F  T  I  S  A  D  T  S  K  N  T  A  Y
        ^CDR-H2
```

```
1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTA GCCGCTGGGG AGGGGACGGC TTCTATGCTA TGGACTACTG GGGTCAAGGA
     GGATGTTTAC TTGTCGAATT CTCGACTCCT GTGACGGCAG ATAATAACAT CGGCGACCCC TCCCCTGCCG AAGATACGAT ACCTGATGAC CCCAGTTCCT
  81  L  Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  S  R  W  G  G  D  G  F  Y  A  M  D  Y  W  G  Q  G
                                                                                            ^CDR-H3
```

```
1701 ACACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT
     TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGTGGGG GGACCGTGGG AGGAGGTTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA
 114  T  L  V  T  V  S  S  A  S  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C
```

```
1801 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC
     CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG
 148  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S
```

```
1901 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG
     TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC
 181  G  L  Y  S  L  S  S  V  V  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K
```

```
2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC ACCTCAGTGG CGGTGGCTCT GGTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA
     CAGCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTTGAG TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGCGAT
 214  V  D  K  K  V  E  P  K  S  C  D  K  T  H  L  S  G  G  G  S  G  G  G  S  G  D  F  D  Y  E  K  M  A  N  A  N
                                                          ^end of heavy chain
                                                               ^start of gene III coat protein (267-end)
```

```
2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGCGCT ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA
     TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTTGCGCGA TGTCAGACTG CGATTTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT
 248  K  G  A  M  T  E  N  A  D  E  N  A  L  Q  S  D  A  K  G  K  L  D  S  V  A  T  D  Y  G  A  A  I  D
```

FIG._25 c

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2201 TGGTTTCATT GGTGACGTTT CCGGCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT
     ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAAACG AGGGTTACC  GAGTTCAGCC ACTGCCACTA
281  G   F   I   G   D   V   S   G   L   A   N   G   N   G   A   T   G   D   F   A   G   S   N   S   Q   M   A   Q   V   G   D   G   D

2301 AATTCACCTT TAATGAATAA TTTCCGTCAA TATTTACCTT CCCTCCCTCA ATCGGTTGAA TGTCGCCCTT TTGTCTTTAG CGCTGGTAAA CCATATGAAT
     TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAG GGAGGGAGT  TAGCCAACTT ACAGCGGGAA AACAGAAATC GCGACCATTT GGTATACTTA
314  N   S   P   L   M   N   N   F   R   Q   Y   L   P   S   V   E   C   R   P   F   F   V   F   S   A   G   K   P   Y   E   F

2401 TTTCTATTGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT CTTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT
     AAAGATAACT AACACTGTTT TATTTGAATA AGGCACCACA GAAACGCAAA GAAAATATAC AACGGTGGAA ATACATACAT AAAAGATGTA AACGATTGTA
348  S   I   D   C   D   K   I   N   L   F   R   G   V   F   A   F   L   L   Y   V   A   T   F   M   Y   V   F   S   T   F   A   N   I

2501 ACTGCGTAAT AAGGAGTCTT AATCATGCCA GTTCTTTTGG CTAGCGCCGC CCTATACCTT GTCCTGCCCTCC CCGGCGTTGCG TCGCGGGTGCA TGGAGCCGGG
     TGACGCATTA TTCCTCAGAA TTAGTACGGT CAAGAAAACC GATCGCGGCG GGATATGGAA CAGACGGGAG GGCGCAACGC AGCGCCACGT ACCTCGGCCC
381  L   R   N   K   E   S   Q

2601 CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT CAATTCTTGC GGAGAACTGT GAATGGCGAA
     GGTGGAGCTG GACTTACCTT CGGCCGCCGT GGAGCGATTG CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAACG CCTCTTGACA CTTACGCGTT

2701 ACCAACCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT CCAGCAGCCG CACGCGGCGC ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCGCATGA
     TGGTTGGGAA CCGTCTTGTA TAGGTAGCGC AGGCGGTAGA GGTCGTCGGC GTGCGCCGCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT

2801 TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGGCGGG TTGCCTTACT GGTTAGCAGA ATGAAATCACC GATACGCGAG CGAACGTGAA GCGACTGCTG
     AGCACGAGGA CAGCAACTCC TGGGCCGATC CGACCCGCCC AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC

2901 CTGCAAAACG TCTGCGACCT GAGCCAACAAC ATGAAATGGTC TTCGGTTTCC GTGTTCGTTA AAGCTCGGAA ACGCGGAAGT CAGCGCCCTG CACCATTATG
     GACGTTTTGC AGACGCTGGA CTCGGTTGTTG TACTTACCAG AAGCCAAAGG CACAAAGCAT TTCAGACCTT TGCGCCTTCA GTCGCGGGAC GTGGTAATAC

3001 TTTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTGTG GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATT TTTTCTGGTT
     AAGGCCTAGA CGTAGCGTCC TACGACGACC GATGGGGACAC CTTGTGGATG TAGACATAAT TGCTTCGCGA CCGTAACTGG GACTCACTAA AAAGAGACCA
```

FIG._25D

```
101 CCCGCCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT
    GGGCGGCGTA GGTATGGCGG TCAACAAATG GGAGTGTTGC AAGGTCATTG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA

201 CATCGGTATC ATTACCCCCA TGAACAGAAA TCCCCCCTTA CACGGAGGCA TCAAGTGACC AAACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA
    GTAGCCATAG TAATGGGGGT ACTTGTCTTT AGGGGGGAAT GTGCCTCCGT AGTTCACTGG TTTGTCCTTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT

301 GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT GGACGCGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA
    CTTCGGTCTG TAATTGCGAA GACCTCTTTG AGTTGCTCGA CCTGCGCCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGCGAC TACTCGAAAT

401 CCGCAGGATC CGGAAATTGT AAACGTTAAT ATTTGTTAA AATTCGCGTT TAAAATCAGCT CATTTTTTGT CCAATAGGCC GAAATCGGCA
    GGCGTCCTAG GCCTTTAACA TTTGCAATTA TAAAACAATT TTAAGCGCAA AATTTTAGTCGA GTAAAAAAT CGGTTATCCGG CTTTAGCCGT

501 AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT GAGTGTTGTT CCAGTTTGGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA
    TTTAGGGAAT ATTTAGTTTT CTTATCTGGC TCTATCCCAA CTCACAACAA GGTCAAACCT TGTTCTCAGG TGATAATTTC TTGCACCTGA GGTTGCAGTT

01  AGGGCGAAAA ACCGTCTATC AGGGCTATGG CCCACTACGT GAACCATCAC CCTAAATCAAG TTTTTTGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC
    TCCCGCTTTT TGGCAGATAG TCCCGATACC GGGTGATGCA CTTGGTAGTG GGATTAGTTC AAAAAACCCC AGCTCCACGG CATTTCGTGA TTTAGCCTTG

701 CCTAAAGGGA GCCCCCGATT TAGAGCTTGA CGGGGAAAGC CGGCGAACGT GGCGAGAAAG GAAGGGAAGA AAGGGAAAGG AGCGGGCGCT AGGGCGCTGG
    GGATTTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTCG GCCGCTTGCA CCGCTCTTTC CTTCCCTTCT TTCGGCTTTCC TCGCCCGCGA TCCCGCGACC

01  CAAGTGTAGC GGTCACGCTG CGCGTAACCA CCACACCCGC CGCGCTTAAT GCGCCGCTAC AGGGCGCGTC CGGATCCTGC CTCGCGCGTT TCGGTGATGA
    GTTCACATCG CCAGTGCGAC GCGCATTGGT GGTGTGGGCG GCGCGAATTA CGCGGCGATG TCCCGCGCAG GCCTAGGACG GAGCGCGCAA AGCCACTACT

01  CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT
    GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG TGTCGAACAG ACATTCGCCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGCG CAGTCGCCCA

01  GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATACT GGCTTAACTA TGCGGCATCA GAGCAGAGATTG TACTGAGAGT
    CAACCGCCCA CAGCCCCGCG TCGGTACTGG GTCAGTGCAT CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA
```

FIG._25E

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4101  GCACCATATG CGGTGTGAAA TACCGCACAG ATGGGTAAGG AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
      CGTGGTATAC GCCACACTTT ATGGCGTGTC TCTTTTATGG CGTAGTCCGC AGGAGCCGAG GACTGAGCGA CGGCGAGCCAG

4201  GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC
      CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCCGCC ATTATGCCAA TAGGTGTCTT AGTCCCCTAT TGCGTCCTTT CTTGTACACT CGTTTTCCGG

4301  AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG
      TCGTTTTCCG GTCCTTGGCA TTTTTTCCGGC GCAACGACCG TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTGCGA GTTCAGTCTC

4401  GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG
      CACCGCTTTG GGCTGTCCTG ATATTTCTAT GGTCCGCAAA GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG ACGGCGAATG GCCTATGGAC

4501  TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC
      AGGCGGAAAG AGGGGAAGCCC TTCGCACCGC GAAAGAGTAT CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACACG

4601  ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC
      TGCTTGGGGG GCAAGTCGGG CTGGCGACGC GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTC TGTGCTGAAT AGCGGTGACC GTCGTCGGTG

4701  TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC
      ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG

4801  TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC
      ACGCGGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCG

4901  AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT
      TCGTCTAATG CGCGTCTTTT TTTCCTAGAG TTCTTCTAGG AAACTAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA

5001  GGTCATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC
      CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA AATTTAATTT TTACTTCAAA ATTTCATTTG ATTTCATATA TACTCATTTG AACCAGACTG
```

FIG._25F

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5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC
     TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG

5201 GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC
     CCCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG

5301 CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC
     GCTCGCGTCT TCACCAGGAC GTTGAAATAG GCGGAGGTAG GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCG

5401 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT
     TTGCAACAAC GGTAACGACG TCCGTAGCAC GCAGCAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA

5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT
     GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA

5601 GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT
     CGTATTAAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGGTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA

5701 TGCTCTTGCC CGGCGTCAAC ACGGGGATAAT ACCGCGCCAC ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA
     ACGAGAACGG GCCGCAGTTG TGCCCTATTA TGGCGCGGTG TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTTGAGAGTT

5801 GGATCTTACC GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT TACTTTCACC AGCGTTTCTG GGTGAGCAAA
     CCTAGAATGG CGACAACTCT AGGTCAAGCT ACATTGGGTG AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAAGAC CCACTCGTTT

5901 AACAGGAAGG CAAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG
     TTGTCCTTCC GTTTTTACGG CGTTTTTCCC TTATTCCCGC TGTGCCTTTA CAACTTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAAATAGTC

6001 GGTTATTGTC TCATGAGCGG ATACATATTT AGAAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG AAAAGTGCCA CCTGACGTCT
     CCAATAACAG AGTACTCGCC TATGTATAAA TCTTTTTATT TGTTTATCCC CAAGGCGCGT GTAAAGGGGC TTTTCACGGT GGACTGCAGA
```

FIG.__25. G

```
101  AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG
     TTCTTTGGTA ATAATAGTAC TGTAATTGGA TATTTTTATC CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC

201  AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGCT CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTCCACT
     TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCAAAGGTGA

301  TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC AGTAGAAAGG GCTTCATCAT ATCAAATGCA AAATAGGGCT TCTGACCTGT
     ACTGTGAAAC TAGGGACTAC CTTTTTGCGTA TTAGACCCTG TCATCTTTCC CGAAGTAGTA TAGTTTACGT TTTATCCCGA AGACTGGACA

101  GAAGCAACAG TTTGTATAAG ACAAACTATC TCACACATCG ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAAT
     CTTCGTTGTC AGTTACCCGT AAACATATTC TGTTTGATAG AGTGTGTAGC TCTGGAAAG ATCTCTACA TGTCACTTTA

501  CCCCGAAATT ATACACATGA CTGAAGGAAG GGAGCTCGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC
     GGGGCTTTAA TATGTGTACT GACTTCCTTC CCTCGAGCAG TGGATTGTAG TGACAATGAA ATTTTTTCAA AGGTGAACTG

01   ACTTTGATCC CTGATGGAAA ACGCATAATC TGGGACAGTA CATCATATCA AATGCAACGT ACAAAGAAAT AGGGCTTCTG ACCTGTGAAG
     TGAAACTAGG GACTACCTTT TGCGTATTAG ACCCTGTCAT GTAGTATAGT TTACGTTGCA TGTTTCTTTA TCCCGAAGAC TGGACACTTC

701  CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAAATCC
     GTTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTCTACATG TCACTTTAGG

801  CCGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTTACTTTA AAAAAGTTTC CACTTGACAC
     GGCTTTAATA TGTGTACTGA CTTCCTTCCC TCGAGCAGTA AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACTGTG

01   TTTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTAGA AAGGGCTTCA TCATATCAAA TGCAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA
     AAACTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCATCT TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCGT

01   ACAGTCAATG GCCATTGTA TAAGACAAAC TATCTCACAC ATCGACAAAC CAATACAAATC
     TGTCAGTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG GTTATGTTAG
```

FIG.__ 25 H

```
  1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTGTATTT GTTGTGTATT AAGCTTGCCC AAAAAGAGAA AGAGTTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAAATGCT TCGCAAATATG GCGGCAAAATG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTTACGA AGCGTTTACGA CGGCGTTTACGA CGGTTGTCGC GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGAGGATACG AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGTCTATGC TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT TGTTTTTATT TTTGTAACTA GTACGCAAGT
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA ACAAAAATAA AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTTATG AAAAAGAATA TCGCATTTCT ATGTTCGTTT TTTCTATTGC TACAAATGCC
    AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAAAATAC TTTTCTTTAT AGCGTAAAGA TACAAGCAAA AAAGATAAACG ATGTTTACGG

  1                                                                  M  K  K  N  I  A  F  L  A  S  M  F  V  F  S  I  A  T  N  A
                                                                    ^start of stII sequence

501 TATGCATCCG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA
    ATACGTAGGC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT

 22  Y  A  S  D  I  Q  M  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T
     ^light chain start                                                                        ^CDR-L1

601 CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG
    GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC

 56  A  V  A  W  Y  Q  Q  K  P  G  K  A  P  K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G
                    ^CDR-L2

701 TAGCGGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAT CTTATACTAC TCCTCCCACG
    ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTA GAATATGATG AGGAGGGTGC

 89  S  G  S  G  T  D  F  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  S  Y  T  T  P  P  T
                                                                        ^CDR-L3
```

FIG._26A

```
1 TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCCT
  AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACG GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA
2 F  G  Q  G   T  K  V   E  I  K    R  T  V     A  A  P  S   V  F  I   F  P  P  S  D  E  Q    L  K  S    G  T  A  S

1 CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTCAC
  GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG
6 V  V  C    L  L  N     N  F  Y  P   R  E  A    K  V  Q    W  K  V  D   N  A  L    Q  S  G    N  S  Q  E   S  V  T

1 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC
  TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
9 E  Q  D    S  K  D  S   T  Y  S    L  S  S    T  L  T  L   S  K  A    D  Y  E    K  H  K  V   Y  A  C    E  V  T

1 CATCAGGGCC TGAGCTCGGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTCCGGC GGTAAGGACC
  GTAGTCCCGG ACTCGAGCGGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG
2 H  Q  G  L   S  S  P    V  T  K    S  F  N  R   G  E  C    G  A  S    S  G  M  A  D  P  N    R  F  R    G  K  D  L
```

^end of light chain, start of gD tag

```
1 TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGGCATCG TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTTGAGTG ATTTATGAA
  ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC ACCGGGATCA TGCGTTCAAG TGCATTTTTC CCAATTGATCT CCAACTCCAC TAAAATACTT
6 A  O                                                                                        M  K
3
```

^start of stII

```
1 AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG
  TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC
1 K  N  I    A  F  L  L   A  S  M    F  V  F    S  I  A  T   N  A  Y    A  E  V    Q  L  V  E   S  G  G    G  L  V
```

^start of heavy chain

```
1 CAGCCAGGGG GCTCACTCCG TTTGTCCCTGT GCAGCTTCTG GCTTCAACAT TAAAGACACC TATATACACT GGGTGCGTCA GGCCCCGGGT AAGGGCCTGG
  GTCGGTCCCC CGAGTGAGGC AAACAGGGACA CGTCGAAGAC CGAAGTTGTA ATTTCTGTGG ATATATGTGA CCCACGCAGT CCGGGGCCCA TTCCCGGACC
3 Q  P  G  G   S  L  R    L  S  C    A  A  S    G  F  N  I   K  D  T    Y  I  H  W  V  R  Q    A  P  G    K  G  L  E
```

^CDR-H1

FIG._26B

```
1501 AATGGGTTGC AAGGATTTAT CCTACGAATG GTTATACTAG ATATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC
     TTACCCAACG TTCCTAAATA GGATGCTTAC CAATATGATC TATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCGCGT CTGTGTAGGT TTTTGTGTCG
  47  W   V   A   R   I   Y   P   T   N   G   Y   T   R   Y   A   D   S   V   K   G   R   F   T   I   S   A   D   T   S   K   N   T   A
               ^CDR-H2

1601 CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC GTCTATTATT GTAGCCGCTG GGGAGGGGAC GGCTTCTATG CTATGGGACTA CTGGGGTCAA
     GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG CAGATAATAA CATCGGCGAC CCCTCCCCTG CCGAAGATAC GATACCCAGTT GACCCCCAGTT
  80  Y   L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C   S   R   W   G   G   D   G   F   Y   A   M   D   Y   W   G   Q
                                                                       ^CDR-H3

1701 GGAACACTAG TCACCGTCTC CTCGGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG
     CCTTGTGATC AGTGGCAGAG GAGCCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC
 113  G   T   L   V   T   V   S   S   A   S   T   K   G   P   S   V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L   G

1801 GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCGGT GTCCTACAGTC
     CGACGGACCA GTTCCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGCC AGGATGTCAG
 147  C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S   G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S

1901 CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC
     GAGTCCTGAG ATGAGGGAGT CGTCGCACCA CTGGCACGGG AGGTCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG
 180  S   G   L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q   T   Y   I   C   N   V   N   H   K   P   S   N   T

2001 AAGGTCGACA AGAAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACGGCCG CATGAAACAG CTAGAGGACA AGGTCGAAGA GCTACTCTCC AAGAACTACC
     TTCCAGCTGT TCTTTTCAACT CGGGTTTAGA ACACTGTTTT GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG
 213  K   V   D   K   K   V   E   P   K   S   C   D   K   T   H   G   R   M   K   Q   L   E   D   K   V   E   E   L   L   S   K   N   Y   H
                                                                          ^end of heavy chain, start of leucine zipper

2101 ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTCGG GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAAGAT
     TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC CCTCGCGCCT TTCGAATCAC CGCCACCGAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA
 247  L   E   N   E   V   A   R   L   K   K   L   V   G   E   R   G   K   L   S   G   G   G   S   G   S   G   D   F   D   Y   E   K   M
     end of leucine zipper, start of gene III coat protein (267-end)^
```

FIG._26C

```
2201  GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC TACAGTCTGA CGCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTACGGT
      CCGTTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA CTTTTGCGCG ATGTCAGACT GCGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA
 280   A   N   A   N   K   G   A   M   T   E   N   A   D   E   N   A   L   Q   S   D   A   K   G   K   L   D   S   V   A   T   D   Y   G

2301  GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG
      CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC GATTACCATT ACCACGATGA CCACTAAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAGC
 313   A   A   I   D   G   F   I   G   D   V   S   G   L   A   N   G   N   G   A   T   G   D   F   A   G   S   N   S   Q   M   A   Q   V   G

2401  GTGACGGTGA TAATTCACCT TTAAATGAATA ATTTCCGTCA ATATTTACCT TTAAATGAATA AATGTCGCCCT TTTGTCTTTA GCGCTGGTAA
      CACTGCCACT ATTAAGTGGA AATTTACTTAT TATAAAGGCAGT TATAAATGGA AGGGAGGGAG TTAGCCAACT TACAGCGGGGA AAACAGAAAT CGGCGACCATT
 347   D   G   D   N   S   P   L   M   N   N   F   R   Q   Y   L   P   S   V   E   C   R   P   F   V   F   S   A   G   K

2501  ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAAACTTA TTCCGTGGTG TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG
      TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTTGAAT AAGGCACCAC AGAAAACGCAA CAACGGTGAA AATACATACA TAAAAGATGC
 380   P   Y   E   F   S   I   D   C   D   K   I   N   L   F   R   G   V   F   A   F   L   L   Y   V   A   T   F   M   Y   V   F   S   T

2601  TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GCTAGCGCCG CCCTATACCT TGTCTGCCTC CCCGCCGTGC GTCGCGGTGC
      AAACGATTGT ATGACGCATT ATTCCTCAGA ATTAGTACGG TCAAGAAAAC CGATCGCGGC GGGATATGGA ACAGACGGAG GGGCGGCAACG CAGCGCCACG
 413   F   A   N   I   L   R   N   K   E   S   O

2701  ATGGAGCCGG GCCACCTCGA CCTGAATGGA AGCCGGCGGC ACCTCGCTAA CGGATTCACC TCAATTCTTG CGGAGAACTG
      TACCTCGGCC CGGTGGAGCT GGACTTACCT TCGGCCGCCG TGGAGCGATT GCCTAAGTGG AGTTAAGAAC GCCTCTTGAC

2801  TGAATGCGCA AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC AGCGTTGGGT CCTGGCCACG
      ACTTACGCGT TTGGTTGGGA ACCGTCTTGT ATAGGTAGCG CAGGCGGTAG AGGTCGTCGG GTAGAGCCCG GGACCGGTGC

2901  GGTGCGCATG ATCGTGCTCC TGTCGGTTGAG GACCCGGCTA GGCTGGCGGG GTTGGCCTTAC AATGAATCAC CGATACGCGA GCGAACGTGA
      CCACGCGTAC TAGCACGAGG ACAGCCAACTC CTGGGCCGAT CCGACCGCCC CAACGGAATG TTACTTAGTG GCTATGCGCT CGCTTGCACT

3001  AGCGACTGCT GCTGCAAAAC GTCTGCCGACC TGAGCAACAA CATGAATGGT CTTCGGTTTC CGTGTTTCGT AAAGTCTGGA AACGCGGAAAG TCAGCGCCCT
      TCGCTGACGA CGACGTTTTG CAGACGGCTGG ACTCGTTGTT GTACTTACCA GAAGCCAAAG GCACAAAGCA TTTCAGACCT TTGCGCCTTC AGTCGCGGGA
```

FIG._26D

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3101 GCACCATTAT GTTCCGGATC TGCATCGGCAG GATGCTGCTG GCTACCCTGT GGAACACCTA CATCTGTATT AACGAAGCGC TGGCATTGAT CCTGAGTGAT
     CGTGGTAATA CAAGGCCTAG ACGTAGCGTC CTACGACGAC CGATGGGACA CCTTGTGGAT GTAGACATAA TTGCTTCGCG ACCGTAACTG GGACTGCACTA

3201 TTTTCTCTGG TCCCGCCGCA TCCATACCGC CAGTTGTTTA CCCTCACAAC GTTCCAGTAA CCGGGCATGT TCATCATCAG TAACCCGTAT CGTGAGCATC
     AAAAGAGACC AGGGCGGCGT AGGTATGGCG GTCAACAAAT GGGAGTGTTG CAAGGTCATT GGCCCGTACA AGTAGTAGTC ATTGGGCATA GCACTCGTAG

3301 CTCTCTCGTT TCATCGGTAT CATTACCCCC ATGAACAGAA ATTCCCCCTT ACACGGAGGC ATCAAGTGAC CAAACAGGAA AAAACCGCCC TTAACATGGC
     GAGAGAGCAA AGTAGCCATA GTAATGGGGG TACTTGTCTT TAAGGGGGAA TGTGCCTCCG TAGTTCACTG GTTTGTCCTT TTTTGGCGGG AATTGTACCG

3401 CCGCTTTATC AGAAGCCAGA CATTAACGCT TCTGGAGAAA CTCAACGAGC TGGACGCGGA TGAACAGGCA GACATCTGTG AATCGCTTCA CGACCACGCT
     GGCGAAATAG TCTTCGGTCT GTAATTGCGA AGACCTCTTT GAGTTGCTCG ACCTGCGCCT ACTTGTCCGT CTGTAGACAC TTAGCGAAGT GCTGGTGCGA

3501 GATGAGCTTT ACCGCAGGAT CCGGAAATTG TAAACGTTAA TATTTTGTTA AAAATTCGCGT TCATTTTTTA ACCAAATAGGC
     CTACTCGAAA TGGCGTCCTA GGCCTTTAAC ATTTGCAATT ATAAAAACAAT TTTAAGCGCA AGTAAAAAAT TGGTTATCCG

3601 CGAAATCGGC AAAATCCCTT ATAAATCAAA AGAATAGACC GAGATAGGGT TGAGTGTTGT TCCAGTTTGG AACAAGAGTC CACTATTAAA GAACGTGGAC
     GCTTTAGCCG TTTTAGGGAA TATTTAGTTT TCTTATCTGG CTCTATCCCA ACTCACAACA AGGTCAAACC TTGTTCTCAG GTGATAATTT CTTGCACCTG

3701 TCCAACGTCA AAGGGGCGAAA AACCGTCTAT CAGGGCTATG GCCCACTACG TGAACCATCA CCCTAATCAA GTTTTTTGGG GTCGAGGTGC CGTAAAGCAC
     AGGTTGCAGT TTCCCGCTTT TTGGCAGATA GTCCCGATAC CGGGTGATGC ACTTGGTAGT GGGATTAGTT CAAAAAACCC CAGCTCCACG GCATTTCGTG

3801 TAAATCGGAA CCCTAAAGGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAACG CCGGGCGAAAG GGAAGGGAAG AAAGCGAAAG GAGCGGGCGC
     ATTTAGCCTT GGGATTTCCC TCGGGGGCTA AATCTCGAAC TGCCCGCTTGC GGCCGCTTTC CCTTCCCTTC TTTCGCTTTC CTCGCCCCGCG

3901 TAGGGGCGCTG GCAAGTGTAG CGGTCACGCT GCGCGTAACC ACCACACCCG CCGCGCTTAA TGCGCCGCTA CAGGGGCGCGT CCTCGCGCGT
     ATCCCGCGAC CGTTCACATC GCCAGTGCGA CGCGCATTGG TGGTGTGGGC GGCGCGAATT ACGCGGCGAT GTCCCGCGCA GGAGCGCGCA

4001 TTCGGTGATG ACGGTGAAAA CCTCTGACAC ATGCAGCTCC CGGAGACGGT CACAGCTTGT CTGTAAGCGG ATGCCGGGAG CAGACAAGCC CGTCAGGGCG
     AAGCCACTAC TGCCACTTTT GGAGACTGTG TACGTCGAGG GCCTCTGCCA GTGTCGAACA GACATTCGCC TACGGCCCTC GTCTGTTCGG GCAGTCCCGC

4101 CGTCAGCGGG TGTTGGCGGGG CAGCCATGAC CCAGTCACGT AGCGATAGCG GAGTGTATAC TGGCTTAACT ATGCGGCATC AGAGCAGATT
     GCAGTCGCCC ACAACCGCCC GTCGGTACTG GGTCAGTGCA TCGCTATCGC CTCACATATG ACCGAATTGA TACGCCGTAG TCTCGTCTAA
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FIG._26 E

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4201  GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCCGCACA GATGCGGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCCGC TTCCCTCGCTC ACTGACTCGC
      CATGACTCTC ACGTGGTATA CGCCACACTT TATGGGCGTGT CTACGCCATTC CTCTTTTATG GCGTAGTCCG CGAGAAGGCG AAGGAGCGG   TGACTGAGCG

4301  TGCGGCTCGGT CGTTCGGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG
      ACGCCGAGCCA GCAAGCCGAC GCCGCTCGCC ATAGTCGAGT GAGTTTCCGC CATTATGCCA ATAGGTGTCT TAGTCCCCTA TTGCGTCCTT TCTTGTACAC

4401  AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC
      TCGTTTTCCG GTCGTTTTCC GGTCCTTGGC ATTTTTCCGG CGCAACGACC GCAAAAAGGT ATCCGAGGCG GGGGGACTGC TCGTAGTGTT TTTAGCTGCG

4501  TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGTTCCGACC CTGCCGCTTA CCGGATACCT
      AGTTCAGTCT CCACCGCTTT GGGCTGTCCT GATATTTCTA TGGTCCGCAA AGGGGGACCT TCGAGGGAGC ACAAGGCTGG GACGGCGAAT GGCCTATGGA

4601  CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT
      GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGCACCG CGAAAGAGTA TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA

4701  GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGGCCACTG
      CCCGACACAC GTGCTTGGGG GGCAAGTCGG GCTGGCGACG CGGAATAGGC CATTGATAGC AGAACTCAGG TTGGGCCATT CTGTGCTGAA TAGCCGGTGAC

4801  GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG
      CGTCGTCGGT GACCATTGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG AATGTCTCAAG AACTTCACCA CCGGATTGAT GCCGATGTGA TCTTCCTGTC

4901  TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT
      ATAAACCATA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTTCTCAA CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA

5001  TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT
      ACAAACGTTC GTCGTCTAAT GCGCGTCTTT TTTTCCTAGA GTTCTTCTAG GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA

5101  TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA
      ATTCCCTAAA ACCAGTACTC TAATAGTTTT TCCTAGAAGT GGATCTAGGA AAATTTAATT TTTACTTCAA AATTTAGTTA GATTTCATAT ATACTCATTT

5201  CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT
      GAACCAGACT GTCAATGGTT ACGAATTAGT CACTCCGTGG ATAGAGTCGC TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGGC AGCACATCTA
```

FIG._26F

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5301  AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC CGGCGAGACCC ACGCTCCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA
      TTGATGCTAT GCCCTCCCGA ATGGTAGACC GGGGTCACGA CGTTACTATG GCGCTCTGGG TGCGAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCGGT

5401  GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGGCCTCCAT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGGCCAGTTA
      CGGCCTTCCC GGCTCGCGTC TTCACCAGGA CGTTGAAATA GGCGGAGGTA TTAACAACGG CCCTTCGATC TCATTCATCA AGCGGTCAAT

5501  ATAGTTTGCG CAACGTTGTT GCCATTGCTG CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC GGTTCCCAAC GATCAAGGCG
      TATCAAACGC GTTGCAACAA CGGTAACGAC GTCCGTAGCA AGCAGCAAAC CATACCGAAG TAAGTCGAAG CCAAGGGTTG CTAGTCCGC

5601  AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC CTTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT
      TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCAATCG AGGAAGCCAG GAAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA

5701  ATGGCAGCAC TGCATAAATTC TCTTACTGTC TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC
      TACCGTCGTG ACGTATTAAG AGAATGACAG ATTCTACGAA CCACTCATGA GTTGGTTCAG TAAGACTCTT ATCACATACG

5801  GGCGACCGAG TTGCTCTTGC CCGGCGTCAA CACGGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG
      CCGCTGGCTC AACGAGAACG GGCCGCAGTT GTGCCCTATT ATGGCGCGGT GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCCGC

5901  AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT
      TTTTGAGAGT TCCTAGAATG GCGACAACTC TAGGTCAAGC TACATTGGGT GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAGTG GTCGCAAAGA

6001  GGGTGAGCAA AAACAGGAAG GCAAAAATGCC GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA
      CCCACTCGTT TTTGTCCTTC CGTTTTTACGG CGTTTTTTCC CTTATTCCCG CTGTGCCTTT ACAACTTATG AGTATGAGAA GGAAAAAGTT ATAATAACTT

6101  GCATTATTCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT AGAAAAAATA AACAAATAGG GGTTCCGCGC ACATTCCCCC GAAAAGTGCC
      CGTAAATAGT CCCAATAACA GAGTACTCGC CTATGTATAA ACTTACATAA TCTTTTTTAT TTGTTTATCC CCAAGGGCG TGTAAAGGGG CTTTTCACGG

6201  ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAATA GGCGTATCAC GAGGCCCTTT CGTCTTCAAT ACAGGTAGAC CTTTCGTAGA
      TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATTGG ATATTTTTAT CCGCATAGTG CTCCGGGAAA GCAGAAGTTA TGTCCATCTG GAAAGCATCT

6301  GATGTACAGT GAAATCCCCG AAATTATACA CATGACTGAA GGAAGGGAGC TCGTCAATTCC CTGCCGGGTT ACGTCACCTA ACATCACTGT TACTTTAAAA
      CTACATGTCA CTTTAGGGGC TTTAAATATGT GTACTGACTT CCTTCCCTCG AGCAGTAAGG GACGGCCCAA TGCAGTGGAT TGTAGTGACA ATGAAATTTT
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FIG.—26G

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6401 AAGTTTCCAC TTGACACTTT GATCCCTGAT TAATCTGGGA CAGTAGAAAG GGCTTCATCA TATCAAATGC AACGTACAAA GAAATAGGGC
     TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCTTTTGCGT ATTAGACCCT GTCATCTTTC CCGAAGTAGT TTGCATGTTT CTTTATCCCG

6501 TTCTGACCTG TGAAGCAACA GTCAATGGGC ATTTGTATAA GACAAAACTAT CTCACACATC GACAAAACCAA TACAATACAG GTAGACCTTT CGTAGAGATG
     AAGACTGGAC ACTTCGTTGT CAGTTACCCG TAAACATATT CTGTTTGATA GAGTGTGTAG CTGTTTGGTT ATGTTATGTC GCATCTCTAC

6601 TACAGTGAAA TCCCCGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCCTGC CACCTAACAT CACTGTTACT TTAAAAAAGT
     ATGTCACTTT AGGGGGCTTTA ATATGTGTAC CCCTCGAGCA GTAAGGGACG GCCCAATGCA GTGACAATGA AATTTTTTCA

6701 TTCCACTTGA CACTTTGATC CCTGATGGAA AACGCATAAT CTGGGACAGT AGAAAGGGCT TCATCATATC AAATGCAACG TACAAAGAAA TAGGGCTTCT
     AAGGTGAACT GTGAAACTAG GGACTACCTT TTGCGTATTA GACCCTGTCA TCTTTCCCGA AGTAGTATAG TTTACGTTGC ATCCCGAAGA

6801 GACCTGTGAA GCAACAGTCA ATGGGCATTT GTATAAGACA AACTATCTCA CACATCGACA AACCAATACA ATCTACAGGT AGAGATGTA
     CTGGACACTT CGTTGTCAGT TACCCGTAAA CATATTCTGT TTGATAGAGT GTGTAGCTGT TTGGTTATGT TAGAGTCCA ATCTCTACAT

5901 CAGTGAAATC CCCGAAAATTA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCCG GGTTACGTCA CCTAACATCA CTGTTACTTT AAAAAAGTTT
     GTCACTTTAG GGGCTTTAAT ATGTGTACTG ACTTCCTTCC CTCGAGCAGT AAGGGACGGC CCAATGCAGT GGATTGTAGT GACAATGAAA TTTTTTCAAA

7001 CCACTTGACA CTTTGATCCC TGATGGAAAA CGCATAAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCAACGTA CAAAGAAATA GGGCTTCTGA
     GGTGAACTGT GAAACTAGGG ACTACCTTTT GCGTATTAGA CCCTGTCATC TTTCCCGAAG TAGTATAGTT TACGTTGCAT CCCGAAGACT

7101 CCTGTGAAGC AACAGTCAAT GGGCATTTGT ATAAGACAAA CTATCTCACA CATCGACAAA CCAATACAAT C
     GGACACTTCG TTGTCAGTTA CCCGTAAACA TATTCTGTTT GATAGAGTGT GTAGCTGTTA GGTTATGTTA G
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FIG._24H

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  1  ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
     TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG
  1   M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I  Q  M  T  Q  S  P  S  S  L
                ^met                                                               ^start of light chain
      ^start of stII signal sequence

101  TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC GACGACATCG CTACACAGGT GACGACGTCA
     ACAGGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACGACATCG CTGCTGTAGC GATGTGTCCA CTGCTGCAGT
 35   S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A  V  A  W  Y  Q  Q  K  P  G  K  A  P
                                              ^CDR-L1

201  GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT
     CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA
 68   K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S
                ^CDR-L2

301  CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAC ATTATACTAC TCCTCCCACG TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG
     GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAAATATGATG AGGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101   L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  H  Y  T  T  P  P  T  F  G  Q  G  T  K  V  E  I  K  R  T  V  A
                                      ^CDR-L3

401  CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
     GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135   L  T  I  S  K  A  D  Y  E  Q  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R

601  ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA
     TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT
201   T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R
```

FIG._27A

```
701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC TGGCATAACT CGAGGCCTGAT CCTCTTACGCC GGACGCCATCG
    CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG ACCGTATTGA GCTCCGGACTA GGAGATGCGG CCTGCCTAGC
235  G   E   C   G   A   S   S   G   M   A   D   P   N   R   F   R   G   K   D   L   A   Q
                       ^end of light chain, start of gD tag

801 TGGCCCTAGT ACGCAAGTTC ACGTAACTAGA GGTAACTGAAAAG ATTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
    ACCGGGATCA TGCGTTCAAG TGCATTGATCT CCAATTGACTT TAAAATACTT CGTAAAGAAG AACGTAGATA CAAGCAAAAA
-23  M   K   N   I   A   F   L   L   A   S   M   F   V   F
                                      ^start of stII

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG
    AGATAACGAT GTTTGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC
 -8  S   I   A   T   N   A   Y   A   E   V   Q   L   V   E   S   G   G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A   A   S   G
                       ^start of heavy chain                                                                                    ^CDR-H1

001 GCTTCACCAT TAGTGGTTCT TGGATACACT GGGTGCGTCA GGCCCCCGGGT AAGGGCCTGG AATGGGTTGC TTGGATTGCT CCTTATAGCG GCGCTACTGA
    CGAAGTGGTA ATCACCAAGA ACCTATGTGA CCCACGCAGT CCGGGGGCCCA TTCCCGGACC TTACCCAACG AACCTAACGA GGAATATCGC CGCGATGACT
 27  F   T   I   S   G   S   W   I   H   W   V   R   Q   A   P   G   K   G   L   E   W   V   A   W   I   A   P   Y   S   G   A   T   D
                                                                                        ^CDR-H2

101 CTATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGGGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCCCGT CTGTGTAGGT TTTTGTGTCG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
 60  Y   A   D   S   V   K   G   R   F   T   I   S   A   D   T   S   K   N   T   A   Y   L   Q   M   N   S   L   R   A   E   D   T   A

201 GTCTATTATT GTGCAAGAGA GGGGGGGCTTG TACTGGGTGT TCGACTACTG GGGTCAAGGA ACACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT
    CAGATAATAA CACGTTCTCT CCCCCCCGAAC ATGACCCACA AGCTGATGAC CCCAGTTCCT TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA
 93  V   Y   Y   C   A   R   E   G   G   L   Y   W   V   F   D   Y   W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S
             ^CDR-H3

301 CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC
    GCCAGAAGGG GGACCGTGGG AGGAGGTTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG
127  V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L   G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S
```

FIG._27B

```
1401 GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC TCCCTCAGCA GCGTGCCCTCC
     CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG TCCTGAGATG AGGGAGTCGT CGCACGGGAGG
160  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L  S  S  V  V  T  V  P  S

1501 AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC
     TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC CAGCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTTGAG
193  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K  V  E  P  K  S  C  D  K  T  H

1601 ACCTCAGTGG CGGTGGCTCT GGTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGCGCT
     TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGCGAT TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTTGCGCGA
227  L  S  G  G  G  S  G  S  G  D  F  D  Y  E  K  M  A  N  A  N  K  G  A  M  T  E  N  A  D  E  N  A  L

                                   ^end of heavy chain
                                    ^start of gene III coat protein (267-end)

1701 ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT GGTGACGTTT CCGGCCTTGC TAATGGTAAT
     TGTCAGACTG CGATTTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA
260  Q  S  D  A  K  G  K  L  D  S  V  A  T  D  Y  G  A  A  I  D  G  F  I  G  D  V  S  G  L  A  N  G  N

1801 GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT TAATGAATAA TTTCCGTCAA TATTTACCTT
     CCACGATGAC CACTAAAACG ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA
293  G  A  T  G  D  F  A  G  S  N  S  Q  M  A  Q  V  G  D  G  D  N  S  P  L  M  N  N  F  R  Q  Y  L  P  S

1901 CCCTCCCTCA ATCGGTTGAA TGTCGCCCTT TTGTCTTTAG CGCTGGTAAA CCATATGAAT TTTCTATTGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT
     GGGAGGGAGT TAGCCAACTT ACAGCGGGAA AACAGAAATC GCGACCATTT GGTATACTTA AAAGATAACT AACACTGTTT TATTTGAATA AGGCACCACA
327  L  P  Q  S  V  E  C  R  P  F  V  F  S  A  G  K  P  Y  E  F  S  I  D  C  D  K  I  N  L  F  R  G  V

2001 CTTTTGCGTTT CTTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT ACTGCGTAAT AAGGAGTCTT AA
     GAAAACGCAAA GAAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCATTA TTCCTCAGAA TT
360  F  A  F  L  Y  V  A  T  F  M  Y  V  F  S  T  F  A  N  I  L  R  N  K  E  S  Q
```

FIG._27C

34/75

1   ATGAAAAAGA ATATCGCATT TCTTCTCTGCA TCTATGTTCG TTTTTTTCTAT TGCTACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG
1   M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
    ^met
    ^start of stII signal sequence   ^start of light chain

101 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCCTGTAGC GACGACATCG
    ACAGGCGGGAG ACACCCGCTA AGTGGACGGC AGGTCAGTC CTACACAGTT GTCTTTGGTC CTTCGAGG
35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
                                      ^CDR-L1

201 GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCCTTCTC GCTTCTCTGG TAGGGGTTCC CGAAGAGAC ATCGCCAAGG GGTCAGTCA
    CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGAGACCT CAGGGAAGAG CGAAGAGACC TTACCTGGTAA
68 K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
         ^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAC ATTATACTAC TCCTCCCACG TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG
    GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
                       ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
    GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
    GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG
168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCAGTGTG AGCTTCAACA
    TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTCACAC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

FIG.— 28A

```
701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC TGGCATAACT CGAGGCCTGAT CCTCTCTACGCC GGACGGCATCG
    CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGA          GCTCCGACTA GGAGATGCGG CCTGCGTAGC
235  G   E   C   G   A   S   G   M   A   D   P   N   R   F   R   G   K   D   L   A   O
                                 ^end of light chain, start of gD tag

801 TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTAACTAGA ATTTATGAA  GCATTCCTTC TTGCATCTAT GTTCGTTTTT
    ACCGGGGATCA TGCGTTCAAG TGCATTTTTC CCAATCTCCAC TAAAATACTT CGTAAAGAAG AACGTAGATA CAAGCAAAAA
-23                                              M   K   N   I   A   F   L   L   A   S   M   F   V   F
                                                 ^start of stII

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG
    AGATAACGAT GTTTGCGCAT GCGACTCCAA GTCGACCACC ACCGGACGAC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC
 -8  S   I   A   T   N   A   Y   A   E   V   Q   L   V   E   S   G   G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A   A   S   G
                    ^start of heavy chain                                                                                  ^CDR-H1

101 GCTTCACCAT TAGTAATTAT GGGATACACT TGGGTGCGTCA GGCCCCGGGT AAGGGCCTGG AATGGGTTGG TAGGATTTCT CCTTCTAACG GCTCTACTTA
    CGAAGTGGTA ATCATTAATA CCCTATGTGA CCCACGCAGT  CCGGGGCCCA TTCCCGGACC TTACCCAACC ATCCTAAAGA GGAAGATTGC CGAGATGAAT
 27  F   T   I   S   N   Y   G   I   H   W   V   R   Q   A   P   G   K   G   L   E   W   V   G   R   I   S   P   S   N   G   S   T   Y
                                                                                             ^CDR-H2

101 CTATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGGGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCGCGT CTGTGTAGGT TTTTGTGTCG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
 60  Y   A   D   S   V   K   G   R   F   T   I   S   A   D   T   S   K   N   T   A   Y   L   Q   M   N   S   L   R   A   E   D   T   A

201 GTCTATTATT GTGCAAAATG CTCGGTCAGG TTCGCTTACT GGGGTCAAGG CCCCAGTTCC CGGCCTCCAC CGGCCGTCTCCT CGGTGCTTCC CAAGGGCCCA TCGGTCTTCC AGCCAGAAGG
    CAGATAATAA CACGTTTTAC GAGCCAGTCC AAGCGAATGA CCCCAGTTCC GGGGTCAAGG GCCGGAGGTG GTTCCCGGGT AGCCAGAAGG
 93  V   Y   Y   C   A   K   C   S   V   R   F   A   Y   W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S   V   F   P
            ^CDR-H3
```

FIG._28|B

```
101 CCCTGGCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC
    GGGACCGTGG GAGGAGGTTC TCGTGGAGAC CCCCGTGTCG CCGGGACCCG ACGGACCAGT TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG
.27  L  A  P    S  S  K    S  T  S  G    G  T  A    A  L  G    C  L  V  K    D  Y  F    P  E  P    V  T  V  S    W  N  S

.01 AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCCGGCGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG
    TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA GGGGCCGCAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCACT GGCACGGGAG GTCGTCGAAC
.60  G  A  L    T  S  G  V    H  T  F    P  A  V    L  Q  S  S    G  L  Y    S  L  S    S  V  V  T    V  P  S    S  S  L

.01 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTCGACAAG AAAGTTGAGC CCAAATCTTG TGACAAAACT CACCTTCAGTG
    CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGGT CGTTGTGGTT CCAGCTGTTC TTTCAACTCG GGTTTAGAAC ACTGTTTTGA GTGGAGTCAC
93   G  T  Q  T    Y  I  C    N  V  N    H  K  P  S    N  T  K    V  D  K    K  V  E  P    K  S  C    D  K  T    H  L  S  G
                                                                                            ^end of heavy chain

                                                                     start of gene III coat protein (267-end)^

.01 GCGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC TACAGTCTGA
    CGCCACCGAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA CCGTTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA CTTTTGCGCG ATGTCAGACT
.7   G  G  S    G  S  G    D  F  D  Y    E  K  M    A  N  A    N  K  G  A    M  T  E    N  A  D    E  N  A  L    Q  S  D

.01 CGCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT
    GCGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC GATTACCATT ACCACGATGA
.60  A  K  G    K  L  D  S    V  A  T    D  Y  G    A  A  I  D    G  F  I    G  D  V    S  G  L  A    N  G  N    G  A  T

.01 GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA AATTACACTT AAAGGCAGTT
    CCACTAAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGGA AATTACTTAT TAAAGGCAGT TTAATGTGAA TTTCCGTCAA
93   G  D  F  A    G  S  N    S  Q  M    A  Q  V  G    D  G  D    N  S  P    L  M  N  N    F  R  Q    Y  L  P    S  L  P  Q

.01 AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT
    TTAGCCAACT TACAGCGGGA AAACAGAAAT CGCGACCATT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAAT AAGGCACCAC AGAAACGCAA
27   S  V  E    C  R  P    F  V  F  S    A  G  K    P  Y  E    F  S  I  D    C  D  K    I  N  L    F  R  G  V    F  A  F

.01 TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAA
    AGAAAATATA CAACGGTGGA AATACATACA TAAAAGATGC AAACGATTGT ATGACGCATT ATTCCTCAGA ATT
.60  L  L  Y    V  A  T  F    M  Y  V    F  S  T    F  A  N  I    L  R  N    K  E  S    O
```

FIG.-128C

1   ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1   M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
       ^met
       ^start of stII signal sequence   ^light chain start

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT CAACAGAAAC CAGGAAAAAGC
    GGGACAGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA GTTGTCTTTG GTCCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
                                                 ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
    AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S
              ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAGC AATCTTATAC TACTCCTCCC ACGTTCGGAC AGGGTACCAA AAACGAACTG
    TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT TTTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
                                       ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
    ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT GACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
    CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA CTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
    TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

FIG._29A

01 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
   TGTCCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT
35 R G E   C G A   S S G M   A D P   N R F   R G K D   L A O
                            ^end of light chain, start of gD tag

01 TCGTGGCCCT AGTACGTAAG TTCACGTAAA AAGGGTAACT AGAGGTTGAG GTGATTTAT GAAAAAGAAT ATCGGCATTTC TTCTTGCATC TATGTTCGTT
   AGCACCGGGA TCATGCATTT AAGTGCATTT TTCCCATTGA TCTCCAACTC CACTAAAAATA CTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
23   M K K N   I A F L   L A S   M F V
                                                ^start of stII

01 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGGTCTCACT CCGTTTGTCC TGTGCAGCTT
   AAAAGATAAC GATGTTTGCG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA
.9 F S I A   T N A   Y A E   V Q L V   E S G   G G L   V Q P G   G S L   R L S   C A A S
                                                                                 ^CDR-H1

01 CTGGCTTCAC CATTAGTGGT TCTGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAGGGGC TGGAATGGGT TGGTAGGATT TCTCCTTATG GCGGCAATAC
   GACCGAAGTG GTAATCACCA AGACTATATG TGACCCACGC AGTCCGGGGC CCATTCCCCG ACCTTACCCA AGAGGAATAC CGCCGTTATG
.9 G F T   I S G   S D I H   W V R   Q A P   G K G L   E W V   G R I   S P Y G   G N T
   ^start of heavy chain   ^CDR-H2

11 TAACTAATGCC GATAGCCGTCA AGGGGCCGTTT CACTATAAAGC GCAGACACAT CCAAAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
   ATTGATACGG CTATCGGCAGT TCCCGGCAAA GTGATATTCG CGTCTGTGTA GGTTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
69 N Y A   D S V K   G R F   T I S   A D T S   K N T   A Y L   Q M N S   L R A   E D T

11 GCCGTCTATT ATTGTGCAAG AGTCGGCGGC CTCAAGTTGC TGTTCGACTA CTGGGGTCAA GGAACACTAG TCACCGTCTC CTCGGCCTCC ACCAAGGGCC
   CGGCAGATAA TAACACGTTC TCAGCGCCG GAGTTCAACG ACAAGCTGAT GACCCCAGTT CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCG
2 A V Y Y   C A R   V G G   L K L L   F D Y   W G Q   G T L V   T V S   S A S   T K G P
        ^CDR-H3

1 CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT
   GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA GTTCCTGATG AAGGGGCTTG GCCACTGCCA
6 S V F   P L A   P S S K   S T S   G G T   A A L G   C L V   K D Y   F P E P   V T V

FIG._29 B

```
1401  GTCGTTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC      GACCGTGCCC
      CAGCACCTTG  AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG      CTGGCACGGG
159    S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L              T  V  P

1501  TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC      AGAAAGTTGA GCCCAAATCT TGTGACAAAA
      AGGTCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG      TCTTTCAACT CGGGTTTAGA ACACTGTTTT
192    S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T          K  V  E  P  K  S  C  D  K  T

1601  CTCACGGCCG CATGAAACAG CTAGAGGACA AGGTCGAAGA      AAGAACTACC ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTCGG
      GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT      TTCTTGATGG TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC
226    H  G  R  M  K  Q  L  E  D  K                    V  E  E  L  L  S  K  N  Y  H  L  E  N  E  V  A  R  L  K  K  L  V  G
```

^end of heavy chain, start of leucine zipper

```
1701  GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC GATTTTGATT ATGAAAAGAT      GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT
      CCTCGCGCCT TTCGAATCAC CGCCACCGAG CTAAAACTAA TACTTTTCTA      CCGTTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA
259    E  R  G  K  L  S  G  G  G  S  G  D  F  D  Y              E  K  M  A  N  A  N  K  G  A  M  T  E  N  A  D
```

^end of leucine zipper, gene III coat protein (267-end)

```
1801  GAAAACGCGC TACAGTCTGA CGCCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG      TGGTTGACGTT TCCGGCCTTG
      CTTTTGCGCG ATGTCAGACT GCGGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC      ACCACTGCAA AGGCCGGAAC
292    E  N  A  L  Q  S  D  A  K  G  K  L  D  S  V  A  T  D  Y  G  A  A  I  D  G  F  I  G  D  V  S  G  L  A

1901  CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG      GCTCAAGTCG GTGACGGTGA TAATGAATA ATTCCGTCA
      GATTACCATT ACCACGATGA CCACTAAAAC GACCGAGATT AAGGGTTTAC      CGAGTTCAGC CACTGCCACT ATTACTTAT TAAGGCAGT
326    N  G  N  G  A  T  G  D  F  A  G  S  N  S  Q  M  A  Q  V  G  D      G  D  N  S  P  L  M  N  N  F  R  Q

2001  ATATTTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA      ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA
      TATAAATGGA AGGGAGGGAG TTAGCCAACT TACAGCGGGA AAACAGAAAT CGCGACCATT      TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAAT
359    Y  L  P  S  L  P  Q  S  V  E  C  R  P  F  V  F  S  A  G  K  P  Y  E  F  S  I  D      C  D  K  I  N  L

2101  TTCCGTGGTG TCTTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG      TTTGCTAACA TACTGGCGTAA TAAGGAGTCT TAA
      AAGGCACCAC AGAAAACGCAA AGAAAAATATA CAACGGTGGA AATACATACA TAAAAGATGC      AAACGATTGT ATGACCGCATT ATTCCTCAGA ATT
392    F  R  G  V  A  T  F  M  V  Y  V  S  T  F  A  N  I  L  R  N  K  E  S  O
```

FIG.—29C

```
1    ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
     TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1    M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  S  D  I  Q  M  T  Q  S  P  S  S
        ^start of stII signal sequence
        ^met                                                                    ^light chain start

101  CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
     GGGACAGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
35   L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A  V  A  W  Y  Q  Q  K  P  G  K  A
                                                   ^CDR-L1

201  TCCGAAGCTT CTGATTACT  CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ACTTCACTCT GACCATCAGC
     AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TGAAGTGAGA CTGGTAGTCG
68   P  K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S
                      ^CDR-L2

301  AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAGC AATCTTATAC TACTCCTCCC ACGTTCGGAC AGGGTACCAA AAACGAACTG
     TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT TTTGCTTGAC
101  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  S  Y  T  T  P  P  T  F  G  Q  G  T  K  V  E  I  K  R  T  V
                                         ^CDR-L3

401  TGGCTGCACC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
     ACCGACGTGG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L  N  N  F  Y  P  R  E

501  GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
     CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG
168  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T  Y  S  L  S

601  AGCACCCTGA CGCTGAGCAA GGCTGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
     TCGTGGGACT GCGACTCGTT CCGACTGATG CTCTTTGTGT TTCAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201  S  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N
```

FIG._30A

701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GCCGGACGCA
    TGTCCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CGGCCTGCGT
235 R G E C G A S S G M A D P N R F R G K D L A O
                                      ^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT
    AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
.23   M K K N I A F L L A S M F V
                                                           ^start of stII

01 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
   AAAAGATAAC GATGTTTGCG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA
-9 F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S
                                                                                                      ^CDR-H1

01 CTGGCTTCAC CATTACTAAT TCCGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGCTACTATT TATCCTTATG GCGGCTATAC
   GACCGAAGTG GTAATGATTA AGGCTATATG TGACCCACGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACGATGATAA ATAGGAATAC CGCCGATATG
6 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T
       ^start of heavy chain   ^CDR-H2

01 TTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
   AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTCG CGTCTGTGTA GGTTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
69 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

11 GCCGTCTATT ATTGTGCAAG AGGGGGCGGG ATGGACGGCT ACGTTATGGA CTACTGGGGT CAAGGAACAC TCCTCGGCCC TCCTCCCAAGG
   CGGCAGATAA TAACACGTTC TCCCCCGCCC TACCTGCCGA TGCAATACCT GATGACCCCA GTTCCTTGTG AGGAGCCGGG AGGAGGGTTCC
2 A V Y Y C A R G G G M D G Y V M D Y W G Q G T L V T V S S A S T K G
              ^CDR-H3

1 GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
  CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCGTG GAGACCCCCG TGTCGCCGGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG
6 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

FIG._30/B

42/75

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1401 GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTCAGA GTCCTCCAGA CTCTCACTCCC TCAGCAGCGT GGTGACCGTG
     CCACAGCACC TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGGAAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC
 159 V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L  S  S  V  V  T  V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA
     GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGTT CGGGTCGTTG TGGTTCCAGC TGTTCTTTCA ACTCGGGTTT AGAACACTGT
 192 P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K  V  E  P  K  S  C  D  K

1601 AAACTCACGG CCGCATGAAA CAGCTAGAGA ACAAGGTCAG AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT
     TTTGAGTGCC GGCGTACTTT GTCGATCTCT TGTTCCAGTC TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTTGAACA
 226 T  H  G  R  M  K  Q  L  E  D  K  V  E  L  L  S  K  N  Y  H  L  E  N  E  V  A  R  L  K  L  V
                    ^end of heavy chain, start of leucine zipper

1701 CGGGGAGCGC GGAAAGCTTA GTGGCGGTGG CTCTGGTTCC CTCTGGTTCC GGTGATTTTG ATTATGAAAA GATGGCAAAC GCTAACAAGG GGGCTATGAC CGAAAATGCC
     GCCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG GAGACCAAGG CCACTAAAAC TAATACTTTT CTACCGTTTG CGATTGTTCC CCCGATACTG GCTTTTACGG
 259 G  E  R  G  K  L  S  G  G  G  S  G  S  G  D  F  D  Y  E  K  M  A  N  A  N  K  G  A  M  T  E  N  A
                      ^end of leucine zipper,  start of gene III coat protein (267-end)

1801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTGGTGAC GTTTCCGGCC
     CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAAGGCCGG
 292 D  E  N  A  L  Q  S  D  A  K  G  K  L  D  S  V  A  T  D  Y  G  A  A  I  D  G  F  I  G  D  V  S  G  L

1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCCAA TCGGGTGACGG TGATAATTCA CCTTTAATGA ATAATTTCCG
     AACGATTACC ATTACCACGA TGACCACTAA AACGACCGAG ATTAAGGGTT AGCCCACTGCC ACTATTAAGT GGAAATTACT TATTAAAGGC
 326 A  N  G  N  G  A  T  G  D  F  A  G  S  N  S  Q  M  A  Q  V  G  D  G  D  N  S  P  L  M  N  N  F  R

2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC
     AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAAAACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTTG
 359 Q  Y  L  P  S  L  P  Q  S  V  E  C  R  P  F  V  F  S  A  G  K  P  Y  E  F  S  I  D  C  D  K  I  N

2101 TTATTCCGTG GTGTCTTTGC GTTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA ACATACTGCG TAATAAGGAG TCTTAA
     AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAAATACAT ACATAAAAGA TGCAAACGAT TGTATGACGC ATTATTCCTC AGAATT
 392 L  F  R  G  V  F  A  F  L  L  Y  V  A  T  F  M  Y  V  F  S  T  F  A  N  I  L  R  N  K  E  S  O
```

FIG._30 C

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
  1 M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  S  D  I  Q  M  T  Q  S  P  S  S
    ^met                                              ^light chain start

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
    GGGACAGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
 35 L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A  V  A  W  Y  Q  Q  K  P  G  K  A
                                            ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTCACTCT GGAGTCCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
    AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGAGTGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
 68 P  K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S
                ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAGC AATCTTATAC TACTCCTCCC ACGTTCGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG
    TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  S  Y  T  T  P  P  T  F  G  Q  G  T  K  V  E  I  K  R  T  V
                                      ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
    ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135 A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L  N  N  F  Y  P  R  E

501 GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
    CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG
168 A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T  Y  S  L  S

601 AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
    TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N
```

FIG._31A

```
)1 ACAGGGGAGA GTGTGGTGCC AGCTCCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTTCGAGGCT GATCCTCTAC GCCGGACGCA
   TGTCCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT
 5 R  G  E  C  G  A  S  S  G  M  A  D  P  N  R  F  R  G  K  D  L  A  Q
                                                   ^end of light chain, start of gD tag

 1 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGGCATTTC TTCTTGCATC TATGTTCGTT
   AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTGA TCTCCAACTC CACTAAAAATA CTTTTTCTTA TAGCCGTAAAG AAGAACGTAG ATACAAGCAA
 3                                                     M  K  K  N  I  A  F  L  L  A  S  M  F  V
                                                        ^start of stII

 1 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
   AAAAGATAAC GATGTTTGCG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA
 9 F  S  I  A  T  N  A  Y  A  E  V  Q  L  V  E  S  G  G  G  L  V  Q  P  G  G  S  L  R  L  S  C  A  A  S
                                                                                        ^CDR-H1

 1 CTGGCTTCAC CATTAATAAT TATGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGGTTATATT TCTCCTCCTA GCGGCGCTAC
   GACCGAAGTG GTAATTATTA ATACTATATG TGACCCACGC AGTCCGGGGC ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGCGATG
 5 G  F  T  I  N  N  Y  D  I  H  W  V  R  Q  A  P  G  K  G  L  E  W  V  G  Y  I  S  P  P  S  G  A  T
   ^start of heavy chain                                                            ^CDR-H2

 1 TTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CAAATGAACA AGCCTACCTA CAAAAAACAC AGCCTACCTA TGAGGACACT
   AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTCG CGTCTGTGTA GTTTACTTGT TCGGATGGAT GTTTTTTGTG TCGGATGGAT ACTCCTGTGA
 9 Y  Y  A  D  S  V  K  G  R  F  T  I  S  A  D  T  S  K  N  T  A  Y  L  Q  M  N  S  L  R  A  E  D  T

 1 GCCGTCTATT ATTGTGCAAG AATGGTCGGC GGGTTATGGA CTACCAGCCG TACGCCTCCC CCCAATACCT GATGACCGGG AGGAGTGGCC TCCACCAAGG
   CGGCAGATAA TAACACGTTC TTACCAGCCG CCCAATACCT GATGGTCGGC ATGCGGAGGG GGGTTATGGA CTACTGGCCG AGGTGGTTCC
 2 A  V  Y  Y  C  A  R  M  V  G  M  R  R  G  V  M  D  Y  W  G  Q  G  T  L  V  T  V  S  S  A  S  T  K  G
                      ^CDR-H3

 1 GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
   CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCGTG GAGACCCCCG TGTCGCCGGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG
 6 P  S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C  L  V  K  D  Y  F  P  E  P  V  T
```

FIG._31B

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1401 GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGGTGCC ACCTTCCCGG CTGTCCTACA CTCACTCTCC GTCCTCAGGA GTCCTCAGGA CCACAGCACC TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGGAAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC
 159 V  S  W    N  S  G  A    L  T  S    G  V  H    T  F  P  A    V  L  Q    S  S  G    L  Y  S  L    S  S  V    V  T  V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA
     GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGTT CGGGTCGTTG TGGTTCCAGC TGTTCTTTCA ACTCGGGTTT AGAACACTGT
 192 P  S  S    L  G  T    Q  T  Y    I  C  N  V    N  H  K    P  S  N    T  K  V  D    K  K  V    E  P  K    S  C  D  K

1601 AAACTCACGG CCGCATGAAA CAGCTAGAGG ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT
     TTTGAGTGCC GGCGTACTTT GTCGATCTCC TGTTCCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTTGAACA
 226 T  H  G    R  M  K    Q  L  E  D    K  V  E    E  L  L    S  K  N  Y    H  L  E    N  E  V    A  R  L  K    K  L  V

1701 CGGGGAGGCGC GGAAAGCTTA GTGGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAAA GATGGCAAAC GCTAACAAGG GGGCTATGAC CGAAAATGCC
     GCCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACTAAAAC TAATACTTTT CTACCGTTTG CGATTGTTCC CCCGATACTG GCTTTTACGG
 259 G  E  R  K  L  S    G  G  G    S  G  S    G  D  F  D    Y  E  K    M  A  N    A  N  K  G    A  M  T    E  N  A
                          ^end of leucine zipper
     ^end of heavy chain, start of leucine zipper

1801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTGGTGAC GTTCCGGCC
     CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAGGCCCGG
 292 D  E  N    A  L  Q  S    D  A  K    G  K  L  D    S  V  A    T  D  Y    G  A  A  I    D  G  F    I  G  D    V  S  G  L

1901 TTGCTAATGG TAAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCCAA TGACCACTAA AACGACCGGA ATTAAGGGTT TGAATAATTCA CCTTTAATGA ATAATTTCCG
     AACGATTACC ATTTACCACGA TGACCACTAA AACGACCGAG ATTAAGGGTT ACTGGTGATT AACGACCGGA GAAAATTACT TATTAAAGGC
 326 A  N  G    N  G  A    T  G  D  F    A  G  S    N  S  Q    M  A  Q  V    G  D  G    D  N  S    P  L  M  N    N  F  R

2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGT CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC
     AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGGA GGAAAACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTTG
 359 Q  Y  L    P  S  L  P    Q  S  V    E  C  R    P  F  V  F    S  A  G    K  P  Y    E  F  S  I    D  C  D    K  I  N

2101 TTATTCCGTG GTGTCTTTGC GTTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA ACATACTGCG TAATAAGGAG TCTTAA
     AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAAATACAT ACATAAAAGA TGCAAACGAT TGTATGACGC ATTATTCCTC AGAATT
 392 L  F  R  G    V  F  A    F  L  L    Y  V  A  T    F  M  Y    V  F  S    T  F  A  N    I  L  R    N  K  E  S  Q
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FIG._31C

1   GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTGTATT AAGCTTGCCC AAAAAGAGA AGAGTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GCGCTGCTGC GAGCTGCTGC AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CGCGACGACG CTCGACGACG TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTGTAACTA GTACGCAAGT
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTATG AAAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCGTTT TTTCTATTGC TACAAATGCC
    AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAAATAC TTTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
                                              M K K N I A F L L A S M F V F S I A T N A
                                                 ^start of stII signal sequence

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCCTCTGT GGGCGATAGG GTCACCATCA CCTGCCGTGC CAGTCAGGAT GTGTCCACTG
    ATACGTCTAT AGGTCTACTG GGTCAGGGGC TCGAGGGACA GGCGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCACG GTCAGTCCTA CACAGGTGAC
21   Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
        ^start of light chain   ^CDR-L1
        ^EcoRV

601 CTGTGAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGGCAT CCTTCCTCTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
    GACATCGGAC CATAGTTGTC TTTGGTCCTT TTCGAGGCTT CGAAGACTAA ATGAGCCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
55   V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
                                                            ^CDR-L2

701 CGGTTCCGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTC
    GCCAAGGCCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGGTGCAAG
88   G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
                                                                                    ^CDR-L3

FIG._32A

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1 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA
  CCTGTCCCAT GGTTCCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
1 G Q G T  K V E  I K R  T V A A  P S V  F I F  P P S D  E Q L  K S G  T A S V
          ^KpnI

1 TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC AGTCACCCAT
  AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG TCAGTGGGTA
5 V C L N N  F Y P R  E A K  V Q W  K V D N  A L Q  S G N  S Q E S  V T E

1 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT
  CGTCCTGTCG TTCCTGTCGT GGATGTCGGA GTCGTCGTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA
8 Q D S  K D S T  Y S L  S S T  L T L S  K A D  Y E K  H K V Y  A C E  V T H

1 CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGCGGT AAGGACCTGG
  GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTCGAGG CCATACCGAC TAGGCTTGGC AAAGGCGCCA TTCCTGGACC
  Q G L S  P V  T K S  F N R G  E C G  A S S  G M A D  P N R  F R G  K D L A
                                                  ^end of light chain, start of gD tag

1 CATAAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAAGGGT AACTAGAGGT TTATGAAAAA
  GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCCA TTGATCTCCA ACTCCACTAA AATACTTTTT
0
                                                                                           M K K
                                                                               ^start of stII

1 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGGCGTACGC TGAGGTTCAG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG
  CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCCGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACGTC
  N I A  F L L A  S M F  V F S  I A T N  A Y A  E V Q  L V E S  G G G  L V Q
                                            ^start of heavy chain
                                            ^BsiWi
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FIG._32-B

1401 CCAGGGGGCT CACTCCGTTT GTCCTCTGCA GCTTCTGGCT TCACCATTAG TGGTTCTTGG CCCGGGTAAG GGCCTGGAAT
     GGTCCCCCGA GTGAGGCAAA CAGGAGACGT CGAAGACCGA AGTGGTAATC ACCAAGAACC TATGTGACCC GGGCCCATTC CCGGACCTTA
  14 P G G S   L R L   S C A   A S G F   T I S   G S W   I H W V R Q A   P G K   G L E W
                                                                           ^CDR-H1

1501 GGGTTGCTTG GATTGCTCCT TATAGGCGCG CTACTGACTA TGCCGATAGC GTTCACTTAT AAGGCGCAGAC ACATCCAAAA ACACAGCCTA
     CCCAACGAAC CTAACGAGGA ATATCCGCGC GATGACTGAT ACGGCTATCG CAAGTGAATA TTCGCGTCTG TGTAGGTTTT TGTGTCGGAT
  48 V A W   I A P   Y S G A   T D Y   A D S   V K G R   F T I   S A D   T S K N   T A Y
                      ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTG CAAGAGAGGG GGGCTTGTAC TGGGTGTTCG ACTACTGGGG TCAAGGAACA
     GGATGTTTAC TTGTCGAATT CTCGACTCCT GTGACGGCAG ATAATAACAC GTTCTCTCCC CCCGAACATG ACCCACAAGC TGATGACCCC AGTTCCTTGT
  81 L Q M   N S L R   A E D   T A V   Y Y C A   R E G   G L Y   W V F D   Y W G   Q G T
                                                                    ^CDR-H3

1701 CTAGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC
     GATCAGTGGC AGAGGAGCCG GAGGTGGTTC CCGGGTAGCC AGAAGGGGGA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTCGCCGG GACCCGACGG
 114 L V T V   S S A   S T K   G P S   V F P L   A P S   S K S T   S G G   T A A   L G C L
                                      ^ApaI

1801 TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC AGTCCTCAGG
     ACCAGTTCCT GATGAAGGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGGACTGGT CGCCGCACGT GTGGAAGGGC CGACAGGATG TCAGGAGTCC
 148 L V K D   Y F P   E P V T   V S W   N S G   A L T S   G V H   T F P   A V L Q   S S G

1901 ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTC
     TGAGATGAGG GAGTCGTCGC ACCACTGGCA CGGGAGGTCG TCGAACCCGT GGGTCTGGAT GTAGACGTTG CACTTAGTGT TCGGGTCGTT GTGGTTCCAG
 181 L Y S   L S S V   V T V   P S S   S L G T   Q T Y   I C N   V N H K   P S N   T K V

2001 GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGGTGGCTCT GGTTCCGGTG ATGCTCGGTT GCCGCCGGGC GTTTTTTATG
     CTGTTCTTTC AACTCGGGTT TAGAACACTG TTTTGAGTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TACGAGCCAA CGGCGGCCCG CAAAAAATAC
 214 D K K V   E P K   S C D   K T H L   O

2101 CTAGCGGCCGC CCTATACCTT GTCTGCCTCC CGGCGTTGCG TCGCGGTGCA TGGAGCCGGG CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGCCTAAC
     GATCGCGGCG GGATATGGAA CAGACGGAGG GCCGCAACGC AGCGCCACGT ACCTCGGCCC GGTGGAGCTG GACTTACCTT CGGCCGCCGT GGAGCGATTG

FIG._32C

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2201  GGATTCACCA CTCCAAGAAT TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGCCGCAA ACCAACCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT
      CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAACG CCTCTTGACA CTTACGGCGT TGGTTGGGAA CCGTCTTGTA TAGGTAGCGC AGGCGGTAGA

2301  CCAGCAGCCG CACGCGGCGC ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCCGCATGA TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGGG
      GGTCGTCGGC GTGCGCCGCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGGTACT AGCAGGAGGA CAGCAACTCC TGGGCCGATC CGACCGCCCC

2401  TTGCCTTACT GGTTAGCAGA ATGAATCACC GATACGCGAG CGAACGTGAA TCTGCGGACT GAGCAACAAC ATGAATGGTC
      AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC CTCGTTGTTG TACTTACCAG

2501  TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGCCCTG CAGCGGCCGAAGT CACCATTATG TTCCGGATCT GCATCGCAGG CTACCCTGTG
      AAGCCAAAGG CACAAAGCAT TTCAGACCTT TGCGCCGGGAC GTCGCCGGGAC GTGGTAATAC AAGGCCTAGA CGTAGCGTCC GATGGGACAC

2601  GAACACCTAC ATCTGTATTA ACGAAGGCGCT CTGAGTGATT TTTCTCTGGT CCATACCGCC AGTTGTTTAC CCTCACAACG
      CTTGTGGATG TAGACATAAT TGCTTCCGCGA GACTCACTAA AAAGAGACCA GGTATGGCGG TCAACAAATG GGAGTGTTGC

2701  TTCCAGTAAC CGGGCCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT ATTACCCCCA TGAACAGAAA TTCCCCCTTA
      AAGGTCATTG GCCCGGTACAA GTAGTAGTCA TTGGGCATAG AGAGCGTAGG AGAGAGCAAA TAATGGGGGT ACTTGTCTTT AAGGGGGAAT

2801  CACGGAGGCA TCAAGTGACC AAACAGGAAA AAAACCGCCCT TAACATGGCC CGCTTTATCA GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT
      GTGCCTCCGT AGTTCACTGG TTTGTCCTTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT CTTCGGTCTG TAATTGCGAA GACCTCTTTG AGTTGCTCGA

2901  GGACGCGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA CCGCAGGATC CGGAAATTGT AAACGTTAAT ATTTGTTAA
      CCTGCGCCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGCGAC TACTCGAAAT GGCGTCCTAG GCCTTTAACA TTTGCAATTA TAAACAATT

3001  AATTCGCGTT AAATTTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT
      TTAAGCGCAA TTTAAAAACA TTTAGTCGA GTAAAAAATT GGTTATCCGG CTTTAGCCGT TTTAGGGAAT ATTTAGTTTT CTTATCTGGC TCTATCCCAA

3101  GAGTGTTGTT CCAGTTTGGA ACAAGAGTCC CCAACGTCAA AGGGCGAAAA ACCGTCTATC AGGGCTATGG CCCACTACGT
      CTCACAACAA GGTCAAACCT TGTTCTCAGG TTGCACCTGA TCCCGCTTTT TGGCAGATAG TCCCGATACC GGGTGATGCA
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FIG._32D

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3201  GAACCATCAC CCTAATCAAG TTTTTTGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC CCTAAAGGGA GCCCCCGATT TAGAGCTTGA CGGGGAAAGC
      CTTGGTAGTG GGATTAGTTC AAAAAACCCC AGCTCCACGG CATTTCGTGA TTTAGCCTTG GGATTTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTCG

3301  CGGCGAACGT GGCGAGAAAG GAAGGGAAGA AAGCGGAAAG AGCGGGGGCT AGGGCGCTGG CAAGTGTAGC GGTCACGCTG CGCGTAACCA CCACACCCGC
      GCCGCTTGCA CCGCTCTTTC CTTCCCTTCT TTCGCTTTCC TCGCCCCGGA TCCCGCGACC GTTCACATCG CCAGTGCGAC GCGCATTGGT GGTGTGGGCG

3401  CGGCGCTTAAT GCGGCCGCTAC AGGGCGCGTC CGGATCCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC
      GCGCGGAATTA CGCGGCGGATG TCCCGCGCAG GCCTAGGACG GAGCGCGCAA AGCCACTACT GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG

3501  ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGGCG AGCCATGACC CAGTCACGTA
      TGTCGAACAG ACATTCGCCT ACGGCCCTCG TCTGTTCGGG CAGTCGCCCG CAACCGCCCA CAGCCCCCGC TCGGTACTGG GTCAGTGCAT

3601  GCGATAGCGG AGTGTATACT GGCTTAACTA TGCGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CGGTGTGAAA TACCGCACAG ATGCGTAAGG
      CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA CGTGGTATAC GCCACACTTT ATGGCGTGTC TACGCATTCC

3701  AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG
      TCTTTTATGG CGTAGTCCGC GAGAAGGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCCGCC

3801  TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC
      ATTATGCCAA TAGGTGTCTT AGTCCCCTAT TGCGTCCTTT CTTGTACACT CGTTTTCCGG TCGTTTTCCG GTCCTTGGCA TTTTTCCGGC GCAACGACCG

3901  GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT
      CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGCTGTCCTG ATATTTCTAT GGTCCGCAAA

4001  CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA
      GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG ACGGCGAATG AGGCGGAAAG AGGGAAGCCC TTCGCACCGC GAAAGAGTAT

4101  GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG
      CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC TGCTTGGGGG GCAAGTCGGG CTGGCGACGC GGAATAGGCC

4201  TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT
      ATTGATAGCA GAACTTCAGT TGGGCCATTC TGTGCTGAAT AGCGGTGACC ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA
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FIG.— 3a.E

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4301  ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG
      TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG ACGCGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC

4401  GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC
      CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC CAAACGTTCG TCGTCTAATG CGCGTCTTTT TTTCCTAGAG TTCTTCTAGG

4501  TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT
      AAACTAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA

4601  TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA
      AATTTAATTT TTACTTCAAA ATTTAGTTAG ATTTCATATA TACTCATTTG AACCAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT

4701  TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC
      AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG CCCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG

4801  GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC
      CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG GCTCGCGTCT TCACCAGGAC GTTGAAATAG GCGGAGGTAG

4901  CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT
      GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCG TTGCAACAAC GGTAACGACG TCCGTAGCAC CACAGTGCGA

5001  CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC
      GCAGCAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG

5101  TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT
      AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA CGTATTAAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA

5201  TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC
      AGACACTGAC CACTCATGAG TTGGTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA ACGAGAACGG GCCGCAGTTG TGCCCTATTA TGGCGCGGTG
```

FIG._32F

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5301 ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC GCTGTTGAGA TCCAGTTCGA TGTAACCCAC
     TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT CCTAGAATGG CGACAACTCT AGGTCAAGCT ACATTGGGTG

5401 TCGTGCACCC AACTGATCTT CAGCCATCTT TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG
     AGCAGCTGGG TTGACTAGAA GTCGGTAGAA ATGAAAGTGG TCGCAAAGAC CCACTCGTTT TTGTCCTTCC GTTTTTTCCC TTATTCCCGC

5501 ACACGGAAAT GTTGAATACT CATATCTTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG GGTTATTGTC ATACATATTT GAATGTATTT
     TGTGCCTTTA CAACTTATGA GTATAGAAAG GAAAAAGTTA TAATAACTTC GTAAATAGTC CCAATAACAG TATGTATAAA CTTACATAAA

5601 AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG AAAAGTGCCA CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG
     TCTTTTTATT TGTTTATCCC CAAGGCGCGT GTAAAGGGGC TTTTCACGGT GGACTGCAGA TTCTTTGGTA ATAATAGTAC TGTAATTGGA TATTTTTATC

5701 GCGTATCACG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG AGTGTACAGTG AATTATACAC ATGACTGAAG GAAGGGAGCT
     CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACAGTCAC TTAATATGTG TACTGACTTC CTTCCCTCGA

5801 CGTCATTCCC TGCCGGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTCCCACT TGACACTTTG ATCCCCTGATG AATCTGGGAC
     GCAGTAAGGG ACGGCCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCAAAGGTGA ACTGTGAAAC TAGGGACTAC TTAGACCCTG

5901 AGTAGAAAGG GCTTCATCAT ATCAAATGCA ACGTACAAAG AAATAGGGCT TTTGTATAAG ACAAACTATC
     TCATCTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTTATCCCGA AAACATATTC TGTTGATAG

6001 TCACACATCG ACAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAAT ATACACATGA GGAGCTCGTC
     AGTGTGTAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAAG CATCTCTACA TGTGTACTT CCTCGAGCAG

6101 ATTCCCTGCC GGGTTACGTC ACCTAACATC TAAAAAAGTT TCCACTTGAC ACTTTGATCC CTGATGGAAA TGGGACAGTA
     TAAGGGACGG CCCAATGCAG TGGATTGTAG ATTTTTTCAA AGGTGAACTG TGAAACTAGG GACTACCTTT ACCCTGTCAT

6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAGAAAT AGGGCTTCTG ACCTGTGAAG CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC
     CTTTCCCGAA GTAGTATAGT TTACGTTGCA TCCCGAAGAC TGGACACTTC GTTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG

6301 ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAAATCC CCGAAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT
     TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAAGCA TCTCTACATG TCACTTTAATA TGTGTACTGA CTTCCTTCCC TCGAGCAGTA

6401 TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTTACTTTA AAAAAGTTC CACTTGACAC GATGGAAAC GCATAAATC GGACAGTAGA
     AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACTGTG CTACCTTTTG CGTATTAGAC CCTGTCATCT

6501 AAGGGCTTCA TCATATATCAAA AAAGAAATAG TGCAACGTAC GGCATTCAAG ACAGTCAATG TAAGACAAAC TATCTCACAC TATCCACAC
     TTCCCGAAGT AGTATATAGTTT TTTCTTTATC ACGTTGCATG CCGTAAGTTAC GTCAGTTAC ATTCTGTTTG ATAGAGTGTG

6601 ATCGACAAAC CAATACAATC
     TAGCTGTTTG GTTATGTTAG
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FIG._32 G

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  1  TTCGAGCTCG CCCGACAATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC
     AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCAATAATTA TCATTAGTTA ATGCCCCAGT AATCAAGTAT CGGGTATATA CCTCAAGGCG CAATGTATTG

101  TTACGGTAAA TGGCCCCGCCT GGCTGACCGC CCAACGACCC TCCCATAGTA ACGCCAATAG GGACTTTCCA
     AATGCCATTT ACCGGGGCGA CCGACTGGCG GGTTGCTGGG AGGGTATCAT TGCGGTTATC CCTGAAAGGT

201  TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT
     AACTGCAGTT ACCCACCTCA TAAATGCCAT TTGACGGGTG AACCGTCATG TAGTTCACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA

301  AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC
     TTTACCGGGC GGACCGTAAT ACGGGTCATG TACTGGAATA CCCTGAAAGG ATGAACCGTC ATGTAGATGC ATAATCAGTA GCGATAATGG TACCACTACG

401  GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA
     CCAAAACCGT CATGTAGTTA CCCGCACCTA TCGCCAAACT GAGTGCCCCT AAAGGTTCAG AGGTGGGGTA ACTGCAGTTA CCCTCAAACA AAACCGTGGT

501  AAATCAACGG GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTCGT
     TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAGGCGG GGTAACTGCG TTTACCCGCC ATCCGCACAT GCCACCCTCC AGATATATTC GTCTCGAGCA

601  TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT CCATAGAAGA CACCGGGGACC GATCCAGCGC CCGGCGGCCG GAACGGGGCA
     AATCACTTGG CAGTCTAGCG GACCTCTGCG GTAGGTGCGA CAAAAACTGGA GGTATCTTCT GTGGCCCTGG CTAGGTCGCG GGCCGCCGGC CTTGCCACGT

701  TTGGAACGCG GATTCCCCGT GCCAAGAGTG CGCCTATAGA GTCTATAGGC CCACCCCCTT GGCTTCGTTA GAACGGCGGCT ACAATTAATA
     AACCTTGCGC CTAAGGGGCA CGGTTCTCAC GCGGATATCT CAGATATCCG GGTGGGGGAA CCGAAGCAAT CTTGCGCCGA TGTTAATTAT

801  CATAAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACTCCCAG GTCCAACTGC
     GTATTGGAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CGGAAAGAGA GGTGAGGGTC CAGGTTGACG

901  ACCTCGGTTC TATCGATTGA ATTCCACCAT GGGATGGTCA TGTATCATCC TTTTCTAGT AGCAACTGCA ACTGGAGTAC ATTCAGATAT CCAGATGACC
     TGGAGCCAAG ATAGCTAACT TAAGGTGGTA CCCTACCAGT ACATAGTAGG AAAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG
                              M   G   W   S   C  I  I  L  F  L  V  A  T  A  T  G  V  H   S   D  I  Q  M  T
  1                             ^met                                               ^Start VL
                                                                                                    ^EcoRV
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FIG._33 A

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1001 CAGTCCCCGA GCTCCCTGTC CGCCCTCTGTG GGCGATAGGG TCACCATCAC CTGCCGTGCC AGTCAGGATG TGTCCACTGC TATCAACAGA
     GTCAGGGGCT CGAGGGACAG GCGGGAGACAC CCGCTATCCC AGTGGTAGTG GACGGCACG TCAGTCCTAC ACAGGTGACG ATAGTTGTCT
  25  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A  V  A  W  Y  Q  Q  K
                                                                          ^CDR-L1

1101 AACCAGGAAA AGCTCCGAAG CTTCTGATTT ACTCGGCATC CTTCCTCTAC CTTCTCGCTT CGGTTCCGGGA CGGATTTCAC
     TTGGTCCTTT TCGAGGCTTC GAAGACTAAA TGAGCCGTAG GAAGGAGATG GAAGAGCGAA GCCAAGGCCCT GCCTAAAGTG
  59  P  G  K  A  P  K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S  G  S  G  T  D  F  T
                          ^CDR-L2

1201 TCTGACCATC AGCAGTCTGC AGCCGGAAGA CTTCGCAACT TATTACTGTC AGCAATCTTA TACTACTCCT CCCACGTTCG GACAGGGTAC CAAGGTGGAG
     AGACTGGTAG TCGTCAGACG TCGGCCTTCT GAAGCGTTGA ATAATGACAG TCGTTAGAAT ATGATGAGGA GGGTGCAAGC CTGTCCCATG GTTCCACCTC
  92  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  S  Y  T  T  P  P  T  F  G  Q  G  T  K  V  E
                                                      ^CDR-L3                                        ^KpnI

1301 ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCTTCTCT TGTGTGCCTG CTGAATAACT
     TAGTTTGCTT GACACCGACG TGGTAGACAG AAGTAGAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT GACGAAGAGA ACACACGGAC GACTTATTGA
 125  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L  N  N  F
                ^start human kappa

1401 TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC
     AGATAGGGTC TCTCCGGTTT CATGTCACCT TCCACCTATT GCGGGAGGTT AGCCCATTGA GGGTCCTCTC ACAGTGTCTC GTCCTGTCGT TCCTGTCGTG
 159  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T

1501 CTACAGCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC
     GATGTCGGAG TCGTCGTGGG ACTGCGACTC GTTTCGTCTG ATGCTCTTTG TGTTTCAGAT GCGGACGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG
 192  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V

1601 ACAAAGAGCT TCAACAGGGG AGAGTGTTAA GCTTGGCCGC CATGGCCCAA CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA
     TGTTTCTCGA AGTTGTCCCC TCTCACAATT CGAACCGGCG GTACCGGGTT GAACAAATAA CGTCGAATAT TACCAATGTT TATTTCGTTA TCGTAGTGTT
 225  T  K  S  F  N  R  G  E  C  O
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FIG._33B

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1701  ATTTCACAAA  TAAAGCATTT  TTTTCACTGC  ATTCTAGTTG  TGGTTTGTCC  AAACTCATCA  ATGTATCTTA  TCATGTCTGG  ATCGGGAATT  AATTCGGCGC
      TAAAGTGTTT  ATTTCGTAAA  AAAAGTGACG  TAAGATCAAC  ACCAAACAGG  TTTGAGTAGT  TACATAGAAT  AGTACAGACC  TAGCCCTTAA  TTAAGCCGCG

1801  AGCACCATGG  CCTGAAATAA  CCTCTGAAAG  AGGAACTTGG  TTAGGTATCT  TCTGAGGCGG  AAAGAACCAG  CTGTGGAATG  TGTGTCAGTT  AGGGTGTGGA
      TCGTGGTACC  GGACTTTATT  GGAGACTTTC  TCCTTGAACC  AATCCATAGA  AGACTCCGCC  TTTCTTGGTC  GACACCTTAC  ACACAGTCAA  TCCCACACCT
                                                                ^change from C to T, kill KpnI site

1901  AAGTCCCCAG  GCTCCCCAGC  AGGCAGAAGT  ATGCAAAGCA  TGCATCTCAA  TTAGTCAGCA  ACCAGGTGTG  GAAAGTCCCC  AGGCTCCCCA  GCAGGCAGAA
      TTCAGGGGTC  CGAGGGGTCG  TCCGTCTTCA  TACGTTTCGT  ACGTAGAGTT  AATCAGTCGT  TGGTCCACAC  CTTTCAGGGG  TCCGAGGGGT  CGTCCGTCTT

2001  GTATGCAAAG  CATGCATCTC  AATTAGTCAG  CAACCATAGT  CCCGCCCCTA  ACTCCGCCCA  TCCCGCCCCT  AGTTCCGCCC  ATTCTCCGCC
      CATACGTTTC  GTACGTAGAG  TTAATCAGTC  GTTGGTATCA  GGGCGGGGAT  TGAGGCGGGT  AGGGCGGGGA  TCAAGGCGGG  TAAGAGGCGG

2101  CCATGGCTGA  CTAATTTTTT  TTATTTATGC  AGAGGCCGAG  GCCGCCTCGG  CCTCTGAGCT  ATTCCAGAAG  TAGTGAGGAG  GCTTTTTTGG  AGGCCTAGGC
      GGTACCGACT  GATTAAAAAA  AATAAATACG  TCTCCGGCTC  CGGCGGAGCC  GGAGACTCGA  TAAGGTCTTC  ATCACTCCTC  CGAAAAAACC  TCCGGATCCG

2201  TTTTGCAAAA  AGCTTGGCAC  AGCTTGTTAAC  TGGCCGTCGT  TTTACAACGT  CGTGACTGGG  AAAACCCTGG  CGTTACCCAA  CTTAATCGCC  TTGCAGCACA
      AAAACGTTTT  TCGAACCGTG  ACCGGCAGCA  AAATGTTGCA  GCACTGACCC  TTTTGGGACC  GCAATGGGTT  GAATTAGCGG  AACGTCGTGT

2301  TCCCCCCTTC  GCCAGCTGGC  GTAATAGCGA  AGAGGCCCGC  ACCGATCGCC  CTTCCCAACA  GTTGCGTAGC  CTGAATGGCG  AATGGCGCCT  GATGCGGTAT
      AGGGGGGAAG  CGGTCGACCG  CATTATCGCT  TCTCCGGGCG  TGGCTAGCGG  GAAGGGTTGT  CAACGCATCG  GACTTACCGC  TTACCGCGGA  CTACGCCATA

2401  TTTCTCCCTTA  CGCATCTGTG  CGGTATTTCA  CACCGCATAC  GTCAAAGCAA  CCATAGTACG  CGCCCTGTAG  CGGCGCATTA  AGCGCGGCGG  GTGTGGTGGT
      AAAGAGGGAAT  GCGTAGACAC  GCCATAAAGT  GTGGCGTATG  CAGTTTCGTT  GGTATCATGC  GCGGGACATC  GCCGCGTAAT  TCGCGCCGCC  CACACCACCA

2501  TACGCGCAGC  GTGACCGCTA  CACTTGCCAG  CGCCCTAGCG  CCCGCTCCTT  TCGCTTTCTT  CCCTTCCTTT  CTCGCCACGT  TCGCCGGCTT  TCCCCGTCAA
      ATGCGCGTCG  CACTGGCGAT  GTGAACGGTC  GCGGGATCGC  GGGCGAGGAA  AGCGAAAGAA  GGGAAGGAAA  GAGCGGTGCA  AGCGGCCGAA  AGGGGCAGTT

2601  GCTCTAAATC  GGGGGCTCCC  TTTAGGGTTC  CGATTTAGTG  CTTTACGGCA  CCTCGACCCC  AAAAAACTTG  ATTTGGGTGA  TGGTTCACGT  AGTGGGCCAT
      CGAGATTTAG  CCCCCGAGGG  AAATCCCAAG  GCTAAATCAC  GAAATGCCGT  GGAGCTGGGG  TTTTTGAAC  TAAACCCACT  ACCAAGTGCA  TCACCCGGTA
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FIG._ 32C

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2701 CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTTGGAC TCTTGTTCCA AACTGGAACA ACACTCAACC CTATCTCGGG
     GCGGGACTAT CTGCCAAAAA GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG AGAACAAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC

2801 CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA
     GATAAGAAAA CTAAATATTC CCTAAAACGG CTAAAGCCGG ATAACCAATT TTTTACTCGA CTAAATTGTT TTTAAATTGC GCTTAAAATT GTTTTATAAT

2901 ACGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC
     TGCAAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG GTTGAGGCGA TAGCGATGCA CTGACCCAGT ACCGACGCGG

3001 CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT
     GGCTGTGGGC GGTTGTGGGC GACTGCCCGA ACAGACGAGG GCCGTAGGCG AATGTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA

3101 CAGAGGTTTT CACCGTGCATC ACCGAAACGC GCGAGGCAGT AATTCTTGAAG ACGAAAGGGC CTCGTGATAC GCCTATTTT ATAGGTTAAT GTCATGATAA
     GTCTCCAAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCTTTCCCG GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT

3201 TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT
     ATTACCAAAG AATCTGCGAGT CCACCGTGAA AAGCCCCTT ACACGCGCCT TGGGGATAAA CAAATAAAAA GATTTATGTA AGTTTATACA TAGGCGAGTA

3301 GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT
     CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAGT TGTAAAGGCA CAGCGGGAAT AAGGGAAAAA ACGCCGTAAA

3401 TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA
     ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACTTTC ATTTTCTACG ACTTCTAGTC AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT

3501 GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAAACGTTT TCCAATGATG AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC
     CGCCATTCTA GGAACTCTCA AAAGCGGGGC TTCTTTGCAAA AGGTTACTAC TCGTGAAAAT TTCAAGACGA TACACCGCGC CATAATAGGG CACTACTGCG

3601 CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA
     GCCCGTTCTC GTTGAGCCAG CGGCCGTATGT GATAAGAGTC TTACTGAACC AGGTTACTAC TCGTCAGTGT CTTTTCGTAG AATGCCTACC GTACTGTCAT
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FIG._33 D

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3701 AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC
     TCTCTTAATA CGTCACGACG GTATTGGTAC TCACTATTGT GACGCCGGTT GAATGAAGAC TGTTGCTAGC CTCCTGGCTT CCTCGATTGG CGAAAAAACG

3801 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT
     TGTTGTACCC CCTAGTACAT TGAGCGGAAC TAGCAACCCT TGGCCTCGAC TTACTTCGGT ATGGTTTGCT GCTCGCACTG TGGTGCTACG GTCGTCGTTA

3901 GGCAACAACG TTGCCGCAAAC TATTAACTGG CGAACTACTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA
     CCGTTGTTGC AACGGCGTTTG ATAATTGACC GCTTGATGAA GGGCCGTTGT TAATTATCTG ACCTACCTCC GCCTATTTCA ACGTCCTGGT

4001 CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG
     GAAGACGCGA GCCGGGAAGG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCCGGTCTAC

4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA
     CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCCTC AGTCCGTTGA TACCTACTTG CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT

4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT
     CGTAACCATT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT AAAAATTAAA TTTTCCTAGA TCCACTTCTA GGAAAAACTA

4301 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTTCTGC
     TTAGAGTACT GGTTTTAGGG AATTGCACTC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT CTTTTCTAGT TTCCTAGAAG AACTCTAGGA AAAAAAGACG

4401 GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT
     CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAAACGGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA

4501 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
     GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGGTGAA GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT

4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
     TAGGACAATG GTCACCGACG ACGGTCACCG CTATTCAGCA CAGAATGGCC CAACCTGAGT TCTGCTATCA ATGGCCTATT CCGCGTCGCC AGCCCGACTT
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FIG._33 E

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4701  CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC GCATTGAGAA TACAGCGTGA AGCGGCCACGC TTCCCGAAGG
      GCCCCCCAAG CACGTGTGTC GGGTCGAACC TCGCTTGCTG GATGTGGCTT ATGTCGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC
4801  GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC
      CTCTTTCCGC CTGTCCATAG GCCATTCGCC GTCCCAGCCT TGTCCTCTCG CGTGCTCCCT CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG
4901  GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA CGGCCAGCAA CGCGGGCCTTT TTACGGTTCC
      CCCAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCCGCCTCG GATACCTTTT TGCGGTCGTT GCGCCCGGAAA AATGCCAAGG
5001  TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG
      ACCGGAAAAC GACCGGAAAA CGAGTGTACA AGAAAGGACG CAATAGGGGA CTAAGACACC TATTGGCATA ATGGCGGAAA CTCACTCGAC TATGGCGAGC
5101  CCGCAGCCGA ACGACCGAGC GCAGCGAGTC GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA
      GGCGTCGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCTTC TCGCGGGTTA TGCGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT
5201  TCCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTACC TCACTCATTA GGCACCCCAG GCTTTACACT
      AGGTCGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA
5301  TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTAA
      AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAATT
```

FIG._33F

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  1 ATTCGAGCTC GCCCGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA
    TAAGCTCGAG CGGGCTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT

101 CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC
    GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAAGG

201 ATTGACGTCA ATGGGTGGAG TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG
    TAACTGCAGT TACCCACCTC ATAAATGCCA TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG GGATAACTGC AGTTACTGCC

301 TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG
    ATTTACCGGG CGGACCGTAA TACGGGTCAT GTACTGGAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC

401 CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC
    GCCAAAACCG TCATGTAGTT ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT ACCCTCAAAC AAAACCGTGG

501 AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG
    TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC

601 TTTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCCG GGAACGGTGC
    AAATCACTTG GCAGTCTAGC GGACCTCTGC GGTAGGTGCG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCCGGC CCTTGCCACG

701 ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG ACATCCACTT TGCCTTTCTC TCCACAGGTG AGAACGCGGC TACAATTAAT
    TAACCTTGCG CCTAAGGGGC ACGGTTCTCA CTGCATTCAT GGCGGATATC TGTAGGTGAA ACGGAAAGAG AGGTGTCCAC TCTTGCGCCG ATGTTAATTA

801 ACATAACCTT ATGTATCATA CACATACGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCCTTTCTC TCCACTCCCA GGTCCCAACTG
    TGTATTGGAA TACATAGTAT GTGTATGCTA AATCCACTGT GATATCTTAT TGTAGGTGAA ACGGAAAGAG AGGTGTCCAC CCAGGGTTGAC

901 CACCTCGGTT CTATGCGATTG AATTCCACCA TGGGATGGTC ATGTATCATC CTTTTTCTAG TAGCAACTGC AACTGGAGCG TACGCTGAGG TTCAGCTGGT
    GTGGAGCCAA GATAGCTAAC TTAAGGTGGT ACCCTACCAG TACATAGTAG GAAAAAGATC ATCGTTGACG TTGACCTCGC ATGCGACTCC AAGTCGACCA

  1            M  G  W  S  C  I  I  L  F  L  V  A  T  A  T  G  A  Y  A  E  V  Q  L  V
               ^start signal peptide                              ^start of heavy chain
               ^met                                                ^BsiW1
```

FIG._34A

```
1001  GGAGTCTGGC GGTGGCCTGG TGCAGCCCAGG GGGCTCACTC CGTTTGTCCT GTGCAGCTTC ATTAGTGGT CTTGGATACA CTGGGTGCGT
      CCTCAGACCG CCACCGGACC ACGTCGGGTCC CCCGAGTGAG GCAAACAGGA CACGTCGAAG TAATCACCAA GAACCTATGT GACCCACGCA
  25   E   S   G   G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A   A   S   G   F   T   I   S   G   S   W   I   H   W   V   R
                                                                    ^CDR-H1

1101  CAGGCCCCGG GTAAGGGCCT GGAATGGGTT GCTTGGATTG CTCCTTATAG CGGCGCTACT GACTATGCCG ATAGCGTCAA GGGCCGTTTC ACTATAAGCG
      GTCCGGGGCC CATTCCCGGA CCTTACCCAA CGAACCTAAC GAGGAATATC GCCGCGATGA CTGATACGGC TATCGCAGTT CCCGGCAAAG TGATATTCGC
  58   Q   A   P   G   K   G   L   E   W   V   A   W   I   A   P   Y   S   G   A   T   D   Y   A   D   S   V   K   G   R   F   T   I   S   A
                                          ^CDR-H2

1201  CAGACACATC CAAAAACACA GCCTACCTAC AAATGAACAG CTTAAGAGCT GAGGACACTG CCGTCTATTA TTGTGCAAGA GAGGGGGGCT TGTACTGGGT
      GTCTGTGTAG GTTTTTGTGT CGGATGGATG TTTACTTGTC GAATTCTCGA CTCCTGTGAC GGCAGATAAT AACACGTTCT CTCCCCCCGA ACATGACCCA
  92   D   T   S   K   N   T   A   Y   L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C   A   R   E   G   G   L   Y   W   V
                                                                                        ^CDR-H3

1301  GTTCGACTAC TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT
      CAAGCTGATG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGGAGGT GGTTCCCGGG TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTCGTGGAGA
 125   F   D   Y   W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S   V   F   P   L   A   P   S   S   K   S   T   S
                                                                    ^ApaI

1401  GGGGGCACAG CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT
      CCCCCGTGTC GCCGGGACCC GACGGACCAG TTCCTGATGA AGGGGCTTGG CCACTGCCAC AGCACCTTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA
 158   G   G   T   A   A   L   G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S   G   A   L   T   S   G   V   H   T   F

1501  TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCCTCAG CAGCGTGGTG ACCGTGCCCT CTAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA
      AGGGCCGACA GGATGTCAGG AGTCCTGAGA TGAGGGGAGTC GTCGCACCAC TGGCACGGGA GATCGTCGAA CCCGTGGGTC TGGATGTAGA CGTTGCACTT
 192   P   A   V   L   Q   S   S   G   L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q   T   Y   I   C   N   V   N

1601  TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC CAGCACCTGA ACTCCTGGGG
      AGTGTTCGGG TCGTTGTGGT TCCACCTGTT CTTTCAACTC GGGTTTAGAA CACTGTTTTG AGTGTGTACG GGTGGCACGG GTCGTGGACT TGAGGACCCC
 225   H   K   P   S   N   T   K   V   D   K   K   V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G
```

FIG.—34B

```
1701 GGACCGTCAG TCTTCCTCTT CCCCCCAAAA CCCAAGGACA CCCTCATGAT CTCCCGGACC CTGGAGGTCA CATGCGTGGT GGTGGACGTG AGCCACGAAG
     CCTGGCAGTC AGAAGGAGAA GGGGGGTTTT CCCTCCAGT GGGAGTACTA GAGGGCCTGG GGACTCCAGT GTACGCACCA CCACCTGCAC TCGGTGCTTC
 258   G  P  S  V     F  L  F     P  P  K  D  T     L  M  I     S  R  T     P  E  V  T     C  V  V  V     D  V     S  H  E  D

1801 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT
     TGGGACTCCA GTTCAAGTTG ACCATGCACC TGCCGCACCT CCACGTATTA CGGTTCTGTT TCGGCGCCCT CCTCGTCATG TTGTCGTGCA TGGCCCACCA
 292   P  E  V     K  F  N     W  Y  V  D     G  V  E     V  H  N     A  K  T  K     P  R  E     E  Q  Y     N  S  T  Y     R  V  V

1901 CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA GAAAACCATC
     GTCGCAGGAG TGGCAGGACG TGGTCCTGAC CGACTTACCG TTCCTCATGT TCACGTTCCA GAGGTTGTTT CGGGAGGGTC GGGGGTAGCT CTTTTGGTAG
 325   S  V  L     T  V  L  H     Q  D  W     L  N  G     K  E  Y  K     C  K  V     S  N  K     A  L  P  A     P  I  E     K  T  I

2001 TCCAAAGCCA AAGGGCAGCC CCGAGAACCA CAGGTGTACA CCCTGCCCCC ATCCCGGGAA GAGATGACCA AGAACCAGGT CAGCCTGACC TGCCTGGTCA
     AGGTTTCGGT TTCCCGTCGG GGCTCTTGGT GTCCACATGT GGGACGGGGG TAGGGCCCTT CTCTACTGGT TCTTGGTCCA GTCGGACTGG ACGGACCAGT
 358   S  K  A  K     G  Q  P     R  E  P     Q  V  Y  T     L  P  P     S  R  E     E  M  T  K     N  Q  V     S  L  T     C  L  V  K

2101 AAGGCTTCTA TCCCAGCGAC ATCGCCGTGG AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC GTGCTGGACT CCGACGGCTC
     TTCCGAAGAT AGGGTCGCTG TAGCGGCACC TCACCCTCTC GTTACCCGTC GGCCTCTTGT TGATGTTCTG GTGCGGAGGG CACGACCTGA GGCTGCCGAG
 392   K  G  F  Y     P  S  D     I  A  V  E     W  E  S     N  G  Q     P  E  N  N     Y  K  T     T  P  P     V  L  D  S     D  G  S

2201 CTTCTTCCTC TACAGCAAGC TCACCGTGGA CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC
     GAAGAAGGAG ATGTCGTTCG AGTGGCACCT GTTCTCGTCC ACCGTCGTCC CCTTGCAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTTGGTGATG
 425   F  F  L     Y  S  K  L     T  V  D     K  S  R     W  Q  Q  G     N  V  F     S  C  S     V  M  H  E     A  L  H     N  H  Y

2301 ACGCAGAAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCCTA AAATGAGTGC GCCCAACTTG TTTATTGCAG
     TGCGTCTTCT CGGAGAGGGA CAGAGGCCCA TTTACTCACG CTGCCGGGAT CTCAGCTGGA CGGGTTGAAC AAATAACGTC
 458   T  Q  K  S     L  S  L     S  P  G  K  O

2401 CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT
     GAATATTACC AATGTTTATT TCGTTATCGT AGTGTTTAAA GTGTTTATTT CGTAAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA
```

FIG._34C

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2501  ATCTTATCAT GTCTGGATCG ATCGGGAATT AATTCGGCGC AGCACCATGG CCTGAAATAA AGGAACTTGG TTAGGTACCT TCTGAGGGCG
      TAGAATAGTA CAGACCTAGC TAGCCCTTAA TTAAGCCGCG TCGTGGTACC GGACTTTATT TCCTTGAACC AATCCATGGA AGACTCCGCC

2601  AAAGAACCAT CTGTGGAATG TGTGTCAGTT AGGGTGTGGA AAGTCCCCAG GCTCCCCAGC AGGCAGAAGT ATGCAAAGCA TTAGTCAGCA
      TTTCTTGGTA GACACCTTAC ACACAGTCAA TCCCACACCT TTCAGGGGTC CGAGGGGTCG TCCGTCTTCA TACGTTTCGT AATCAGTCGT

2701  ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGCAGAA GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCCTA ACTCCGCCCA
      TGGTCCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGTCTT CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGAT TGAGGCGGGT

2801  TCCCGCCCCT AACTCCGCCC AGTTCCGCCC ATTCTCCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCCGAG GCCGCCCTCG CCTCTGAGCT
      AGGGCGGGGA TTGAGGCGGG TCAAGGCGGG TAAGAGGCGG GGTACCGACT GATTAAAAAA AATAAATACG TCTCCGGCTC CGGCGGGAGC GGAGACTCGA

2901  ATTCCAGAAG TAGTGAGGAG GCTTTTTTGG AGGCCTAGGC TTTTGCAAAA AGCTGTTAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG
      TAAGGTCTTC ATCACTCCTC CGAAAAAACC TCCGGATCCG AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AAATGTTGCA GCACTGACCC

3001  AAAACCCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCCTTC GCCAGTTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA
      TTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTGT AGGGGGGAAG CGGTCAACCG CATTATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGGTTGT

3101  GTTGCGTAGC CTGAATGGCG AATGGCGCCT GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GTGGCGTATG CCATAGTACG
      CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CACCGCATAC GGTATCATGC

3201  CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
      GCGGGACATC GCCGCGTAAT TCGCGCCGCC CACACCACCA ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGGATCGC GGGCGAGGAA AGCGAAAGAA

3301  CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC
      GGGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT CGAGATTTAG CCCCCGAGGG AAATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGGG

3401  AAAAAACTTG ATTTGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGGAGTC CACGTTCTTT AATAGTGGAC
      TTTTTTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA GCGGGACTAT CTGCCAAAAA GCGGGAAACT GCAACCCTCAG GTGCAAGAAA TTATCACCTG
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FIG._134 ①

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3501 TCTTGTTCCA AACTGGAACA ACACTCAACC CTATTCTTTT GATTTATAAG GGATTTTGCC TATTGGTTAA AAAATGAGCT
     AGAACAAGGT TTGACCTTGT TGTGAGTTGG GATAGAGAAA CTAAAATATTC CCTAAAACGG CTAAAGCCGG ATAACCAATT TTTTACTCGA

3601 GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC
     CTAAATTGTT TTTAAATTGC GCTTAAAATT GTTTTATAAT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG

3701 CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC CCGACACCCG CTGACGCGCC TGTCTGCTCC CGGCATCCGC
     GTTGAGGCGA TAGCCGATGCA CTGACCCAGT ACCGACGCGG GGCTGTGGGC GACTGCGCGG ACAGACGAGG GCCGTAGGCG

3801 TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGT ATTCTTGAAG ACGAAAGGGC
     AATGTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAAA GTGGCAGTAG CGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCTTTCCCG

3901 CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT
     GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT AATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCCTTT ACACGCGCCT TGGGGATAAA

4001 GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA
     CAAATAAAAA GATTTATGTA AGTTTATACA TAGGCGAGTA CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAGT

4101 ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG
     TGTAAAGGCA CAGCGGGAAT AAGGGAAAAA ACGCCGTAAA ACGGAAGGAC GGGTCTTTGC GACCACTTTC ATTTTCTACG ACTTCTAGTC

4201 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA
     AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT CGCCATTCTA GGAACTCTCA AAAGCGGGGC TTCTTGCAAA AGGTTACTAC TCGTGAAAAT

4301 AAGTTCTGCT ATGTGGGCGC GTATTATCCC GTGATGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC
     TTCAAGACGA TACACCCGCG CATAATAGGG CACTACTGCG GCCCGTTCTC GTTGAGCCAG CGGCGTATGT GATAAGAGTC TTACTGAACC AACTCATGAG

4401 ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT. GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG
     TGGTCAGTGT CTTTTCGTAG AATGCCTACC GTACTGTCAT TCTCTTAATA CGTCACGACG GTATTGGTAC TCACTATTGT GACGCCGGTT GAATGAAGAC

4501 ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA
     TGTTGCTAGC CTCCTGGCTT CCTCGATTGG CGAAAAAACG TGTTGTACCC CCTAGTACAT TGAGCGGAAC TAGCAACCCT TGGCCTCGAC TTACTTCGGT
```

FIG._34:E

4601 TACCAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT CCCGGCAACA
      ATGGTTTGCT GCTCGCCACTG TGGTGCTACG GTCGTCGTTA CCGTTGTTGC AACGCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT

4701 ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG
      TAATTATCTG ACCTACCTCC GCCTATTTCA ACGTCCTGGT GAAGACGGCGA CCGACCGAAGG AAATAACGAC TATTTAGACC TCGGCCACTC

4801 CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
      GCACCCAGAG CGCCATAGTA AGTCGTGAC CCCGGTCTAC CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCCTC AGTCCGTTGA TACCTACTTG

4901 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAAACTTCA
      CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT CGTAACCATT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT

5001 TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA
      AAAAATTAAA TTTTCCTAGA TCCACTTCTA GGAAAAACTA TTAGAGTACT GGTTTTTAGGG AATTGCACTC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT

5101 GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG
      CTTTTCTAGT TTCCTAGAAG AACTCTAGGA AAAAAAGACG CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAAACGGCC

5201 ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT
      TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGGTGAA

5301 CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA
      GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT TAGGACAATG GTCACCGACG ACGGTCACCG CTATTCAGCA CAGAATGGCC CAACCTGAGT

5401 AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC
      TCTGCTATCA ATGGCCTATT CCGCGTCGCC AGCCCGACTT GCCCCCCAAG CACGTGTGTC GGGTCGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG

5501 TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA
      ATGTCGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC CTCTTTCCGC CTGTCCATAG GCCATTCGCC GTCCCAGCCT TGTCCTCTCG CGTGCTCCCT

5601 GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC
      CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG CCCAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCGCCTCG

FIG._34:F

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5701 CTATGGAAAA ACGCCAGCAA CGGCGGCCTTT TTACGGTTCC TGGCCTTTTG CTGGCCTTTTG CTGGCCTTTTG GTTATCCCCT GATTCTGTGG
     GATACCTTTT TGCGGTCGTT GCGCCGGAAA AATGCCAAGG ACCGGAAAAC GACCGGAAAA CGAGTGTACA AGAAAGGACG CTAAGACACC

5801 ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGGAGTC AGTGAGCGAG AGCGCCCAAT
     TATTGGCATA ATGGCGGAAA CTCACTCGAC TATGGCGAGC GGCGTCGGCT TGCTGGCTCG CGTCGCCTCAG TCACTCGCTC TCGCGGGTTA

5901 ACGCAAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TCCAACTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT
     TGCGGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT AGGTTGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA

6001 GTGAGTTACC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
     CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAGG CCGAGCATAC AACACTCGCC TATTGTTAAA GTGTGTCCTT

6101 ACAGCTATGA CCATGATTAC GAATTA
     TGTCGATACT GGTACTAATG CTTAAT
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FIG.-34 G

LC Frequency

Pos										
28	S 511	N 262	V 258	D 186	G 178	I 44	T 39	L 16	X 35	
29	I 612	S 272	V 254	G 192	N 147	X 70				
30	S 849	N 176	K 169	G 86	R 81	Y 63	T 29	D 28	A 17	X 45
31	S 676	N 496	T 170	R 47	I 29	D 28	K 25	G 18	X 53	
32	Y 1055	N 128	W 97	F 77	S 61	D 40	R 25	X 69		
50	G 386	A 341	D 294	W 151	K 116	L 91	E 39	S 30	X 82	
53	S 545	N 438	T 407	K 41	I 23	R 23	X 58			
91	Y 849	S 196	R 169	A 118	G 61	H 41	X 148			
92	Y 362	G 356	N 248	S 193	D 114	L 94	T 64	I 38	X 91	
93	S 738	N 346	Q 117	T 101	H 66	G 51	D 47	R 35	X 112	
94	S 386	T 365	W 288	Y 172	L 114	F 79	A 46	P 43	V 33	I 24
96	L 264	Y 205	F 176	F 140	I 117	R 115	P 46	X 121	N 18	X 40

FIG._35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIIK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

FIG._36

Light Chain Designed Diversity
Diversity: ~ 2.9 x 10^9

CDR-L1: diversity ~ 7 x 10^3

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

CDR-L2: diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity ~ 2.3 x 10^4

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			Y	

FIG._37

Light Chain Designed Diversity
Diversity: ~ 6.1 x 10^8

CDR-L1: diversity ~ 3.4 x 10^3

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T		
		V		

CDR-L2: diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity ~ 1.0 x 10^4

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

FIG._38

Light Chain Designed Diversity

CDR-L3: diversity ~ 1.3 x 10³

91	92	93	94	96
TMT	DMC	RVT	WHT	HTT
S	A	A	F	F
Y	D	D	I	I
	N	G	N	L
	S	N	S	
	T	S	T	
	Y	T	Y	

FIG._39

CDR-L1

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		V	V	V
				Y

CDR-L2

50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

CDR-L3

91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

*Amber stop codon is encoded by the degenerate codon

FIG._40
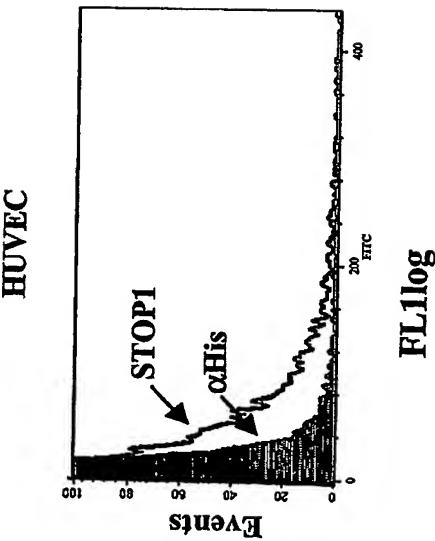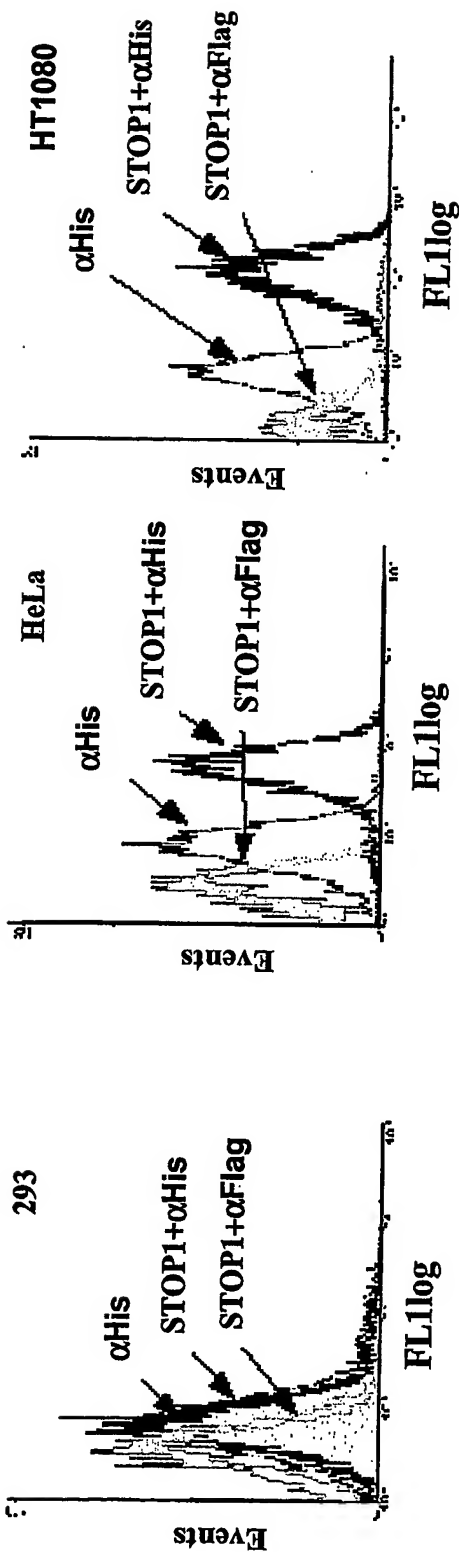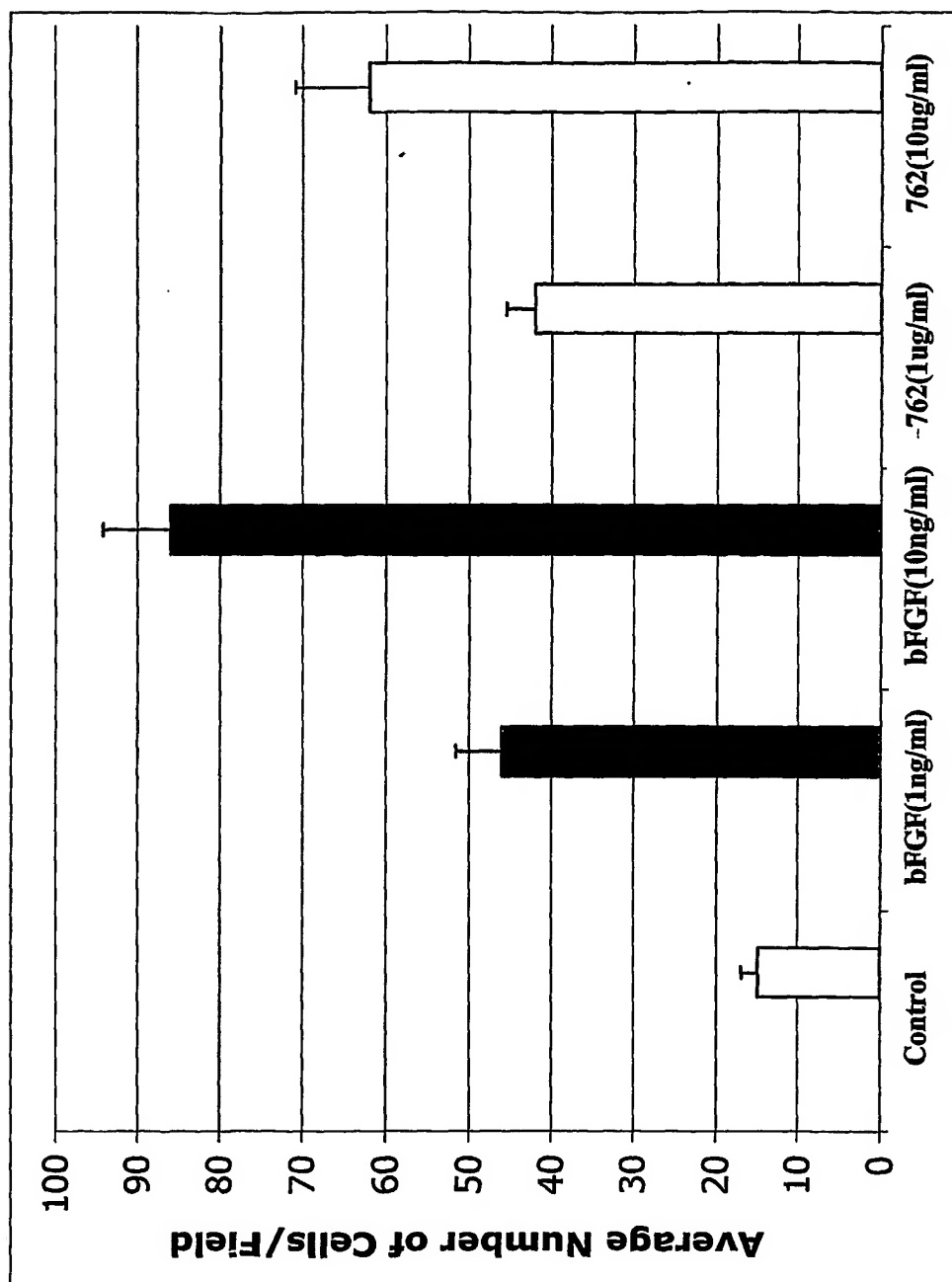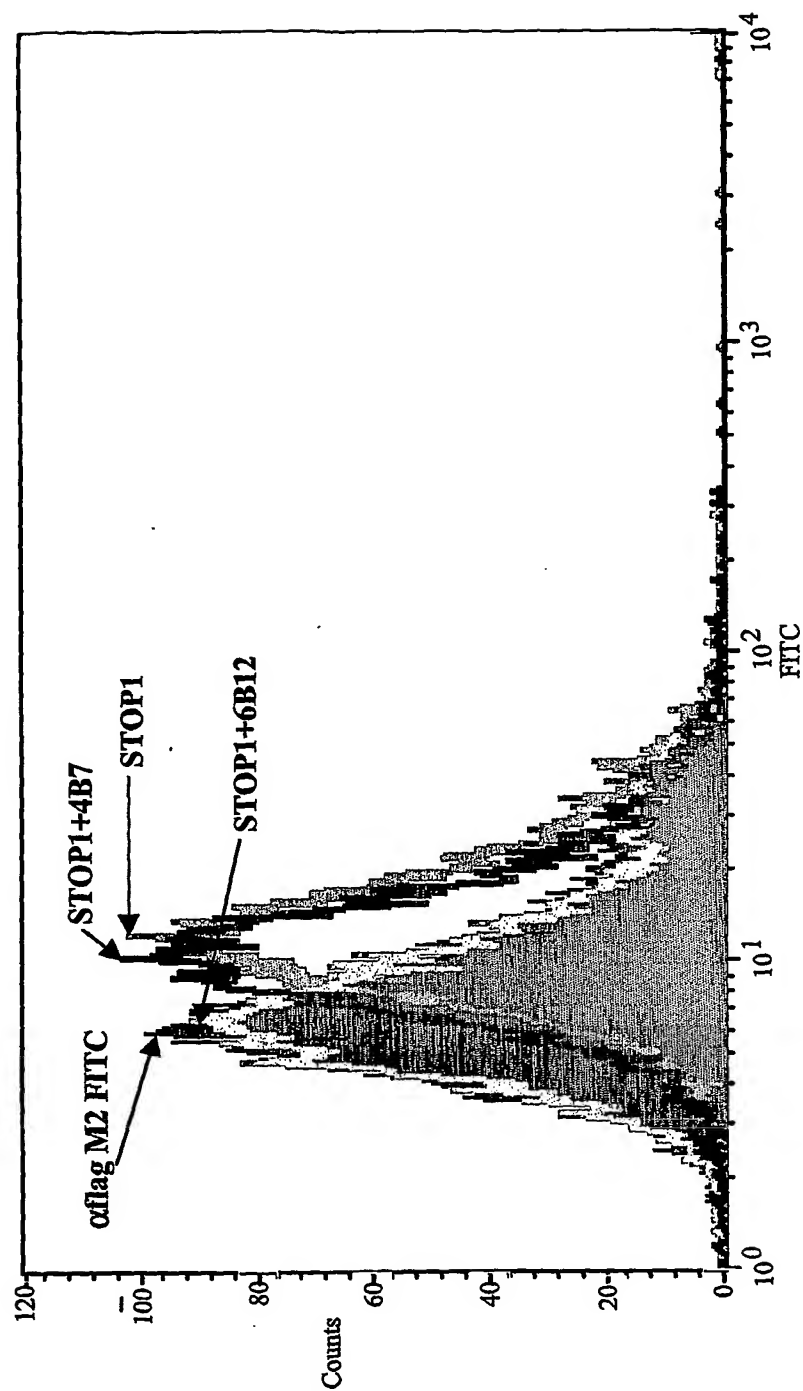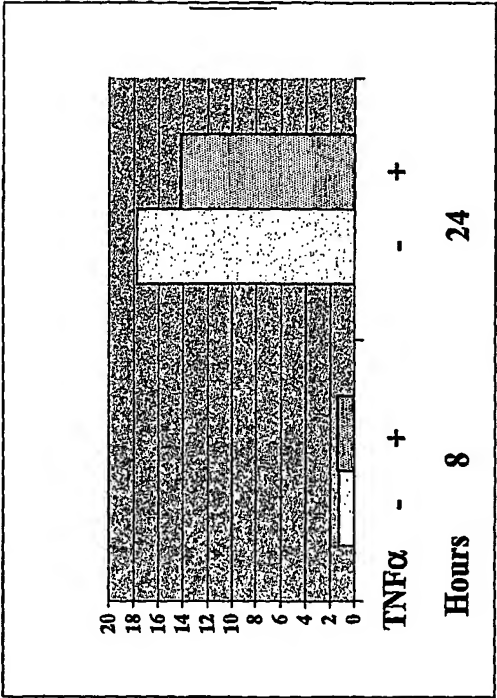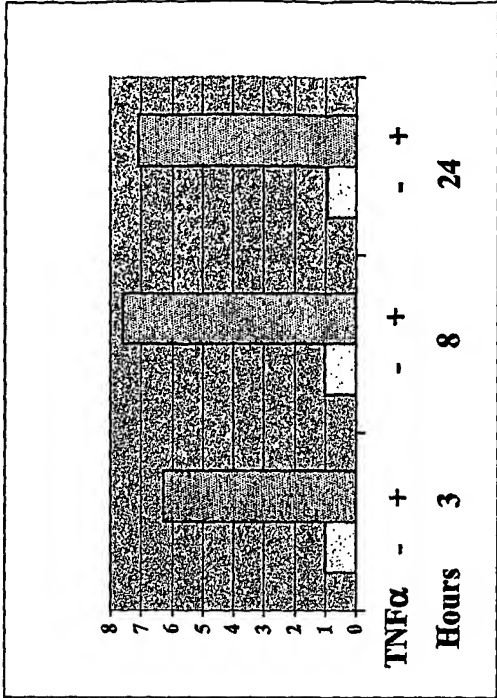
FIG.41
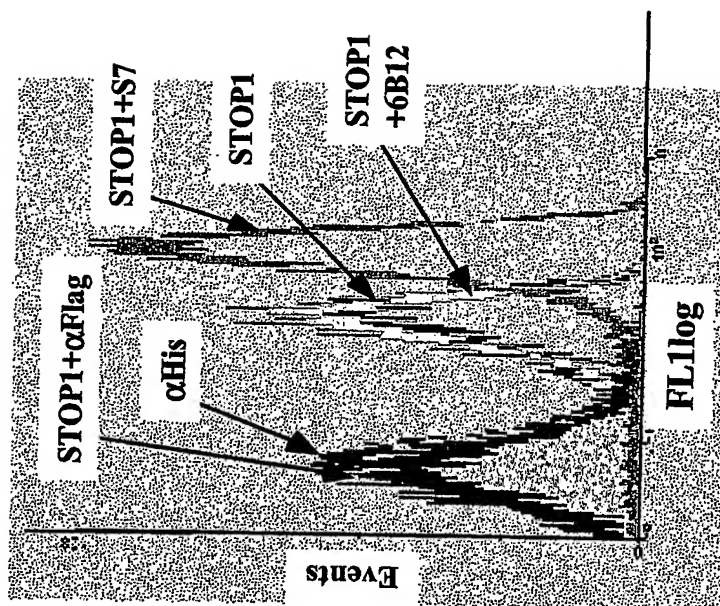
FIG.42

FIG.43

FIG.44

FIG.45

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